

## SEQUENCE LISTING

&lt;110&gt; BASF Plant Science GmbH

<120> Method for Producing Multiple Unsaturated  
Fatty Acids in Plants

&lt;130&gt; 2002/271

&lt;140&gt; 2002\_271

&lt;141&gt; 2002-04-26

&lt;160&gt; 64

&lt;170&gt; PatentIn Vers. 2.0

&lt;210&gt; 1

&lt;211&gt; 1687

&lt;212&gt; DNA

&lt;213&gt; Borago officinalis

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (42) .. (1388)

&lt;223&gt; D6-desaturase

&lt;400&gt; 1

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 Lys Lys Tyr Ile Thr Ser Asp Glu Leu Lys Asn His Asp Lys Pro Gly  
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gat cta tgg atc tcg att caa ggg aaa gcc tat gat gtt tcg gat tgg 152  
 Asp Leu Trp Ile Ser Ile Gln Gly Lys Ala Tyr Asp Val Ser Asp Trp  
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gtg aaa gac cat cca ggt ggc agc ttt ccc ttg aag agt ctt gct ggt 200  
 Val Lys Asp His Pro Gly Gly Ser Phe Pro Leu Lys Ser Leu Ala Gly  
 40 45 50

caa gag gta act gat gca ttt gtt gca ttc cat cct gcc tct aca tgg 248  
 Gln Glu Val Thr Asp Ala Phe Val Ala Phe His Pro Ala Ser Thr Trp  
 55 60 65

aag aat ctt gat aag ttt ttc act ggg tat tat ctt aaa gat tac tct 296  
 Lys Asn Leu Asp Lys Phe Phe Thr Gly Tyr Tyr Leu Lys Asp Tyr Ser  
 70 75 80 85

gtt tct gag gtt tct aaa gat tat agg aag ctt gtg ttt gag ttt tct 344  
 Val Ser Glu Val Ser Lys Asp Tyr Arg Lys Leu Val Phe Glu Phe Ser  
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 Lys Met Gly Leu Tyr Asp Lys Lys Gly His Ile Met Phe Ala Thr Leu

105	110	115	
tgc ttt ata gca atg ctg ttt gct atg agt gtt tat ggg gtt ttg ttt Cys Phe Ile Ala Met Leu Phe Ala Met Ser Val Tyr Gly Val Leu Phe 120 125 130			440
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ctt tgg att cag agt ggt tgg att gga cat gat gct ggg cat tat atg Leu Trp Ile Gln Ser Gly Trp Ile Gly His Asp Ala Gly His Tyr Met 150 155 160 165			536
gta gtg tct gat tca agg ctt aat aag ttt atg ggt att ttt gct gca Val Val Ser Asp Ser Arg Leu Asn Lys Phe Met Gly Ile Phe Ala Ala 170 175 180			584
aat tgt ctt tca gga ata agt att ggt tgg tgg aaa tgg aac cat aat Asn Cys Leu Ser Gly Ile Ser Ile Gly Trp Trp Lys Trp Asn His Asn 185 190 195			632
gca cat cac att gcc tgt aat agc ctt gaa tat gac cct gat tta caa Ala His His Ile Ala Cys Asn Ser Leu Glu Tyr Asp Pro Asp Leu Gln 200 205 210			680
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tct cat ttc tat gag aaa agg ttg act ttt gac tct tta tca aga ttc Ser His Phe Tyr Glu Lys Arg Leu Thr Phe Asp Ser Leu Ser Arg Phe 230 235 240 245			776
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aat gtg tcc tat cga gct cat gaa ctc ttg gga tgc cta gtg ttc tcg Asn Val Ser Tyr Arg Ala His Glu Leu Leu Gly Cys Leu Val Phe Ser 280 285 290			920
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cag ttc tcc ttg aac cac ttc tct tca agt gtt tat gtt gga aag cct Gln Phe Ser Leu Asn His Phe Ser Ser Ser Val Tyr Val Gly Lys Pro 330 335 340			1064

aaa ggg aat aat tgg ttt gag aaa caa acg gat ggg aca ctt gac att 1112  
 Lys Gly Asn Asn Trp Phe Glu Lys Gln Thr Asp Gly Thr Leu Asp Ile  
                   345                  350                  355

tct tgt cct cct tgg atg gat tgg ttt cat ggt gga ttg caa ttc caa 1160  
 Ser Cys Pro Pro Trp Met Asp Trp Phe His Gly Gly Leu Gln Phe Gln  
                   360                  365                  370

att gag cat cat ttg ttt ccc aag atg cct aga tgc aac ctt agg aaa 1208  
 Ile Glu His His Leu Phe Pro Lys Met Pro Arg Cys Asn Leu Arg Lys  
                   375                  380                  385

atc tcg ccc tac gtg atc gag tta tgc aag aaa cat aat ttg cct tac 1256  
 Ile Ser Pro Tyr Val Ile Glu Leu Cys Lys Lys His Asn Leu Pro Tyr  
 390                  395                  400                  405

aat tat gca tct ttc tcc aag gcc aat gaa atg aca ctc aga aca ttg 1304  
 Asn Tyr Ala Ser Phe Ser Lys Ala Asn Glu Met Thr Leu Arg Thr Leu  
                   410                  415                  420

agg aac aca gca ttg cag gct agg gat ata acc aag ccg ctc ccg aag 1352  
 Arg Asn Thr Ala Leu Gln Ala Arg Asp Ile Thr Lys Pro Leu Pro Lys  
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aat ttg gta tgg gaa gct ctt cac act cat ggt taa aattaccctt 1398  
 Asn Leu Val Trp Glu Ala Leu His Thr His Gly  
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ttgttggagt cattgcaact tgtcttttat gggtttattag atgtttttta atatatttta 1518

gaggttttgc tttcatctcc attattgatg aataaggagt tgcattattgt caattgttgt 1578

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<210> 2

<211> 448

<212> PRT

<213> Borago officinalis

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           20                  25                  30

Asp Val Ser Asp Trp Val Lys Asp His Pro Gly Gly Ser Phe Pro Leu  
       35                  40                  45

Lys Ser Leu Ala Gly Gln Glu Val Thr Asp Ala Phe Val Ala Phe His  
       50                  55                  60

Pro	Ala	Ser	Thr	Trp	Lys	Asn	Leu	Asp	Lys	Phe	Phe	Thr	Gly	Tyr	Tyr	
65					70					75					80	
Leu	Lys	Asp	Tyr	Ser	Val	Ser	Glu	Val	Ser	Lys	Asp	Tyr	Arg	Lys	Leu	
				85					90					95		
Val	Phe	Glu	Phe	Ser	Lys	Met	Gly	Leu	Tyr	Asp	Lys	Lys	Gly	His	Ile	
			100					105					110			
Met	Phe	Ala	Thr	Leu	Cys	Phe	Ile	Ala	Met	Leu	Phe	Ala	Met	Ser	Val	
		115					120					125				
Tyr	Gly	Val	Leu	Phe	Cys	Glu	Gly	Val	Leu	Val	His	Leu	Phe	Ser	Gly	
	130					135					140					
Cys	Leu	Met	Gly	Phe	Leu	Trp	Ile	Gln	Ser	Gly	Trp	Ile	Gly	His	Asp	
145					150					155					160	
Ala	Gly	His	Tyr	Met	Val	Val	Ser	Asp	Ser	Arg	Leu	Asn	Lys	Phe	Met	
				165					170					175		
Gly	Ile	Phe	Ala	Ala	Asn	Cys	Leu	Ser	Gly	Ile	Ser	Ile	Gly	Trp	Trp	
			180					185					190			
Lys	Trp	Asn	His	Asn	Ala	His	His	Ile	Ala	Cys	Asn	Ser	Leu	Glu	Tyr	
		195					200					205				
Asp	Pro	Asp	Leu	Gln	Tyr	Ile	Pro	Phe	Leu	Val	Val	Ser	Ser	Lys	Phe	
	210					215					220					
Phe	Gly	Ser	Leu	Thr	Ser	His	Phe	Tyr	Glu	Lys	Arg	Leu	Thr	Phe	Asp	
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Ser	Leu	Ser	Arg	Phe	Phe	Val	Ser	Tyr	Gln	His	Trp	Thr	Phe	Tyr	Pro	
				245					250					255		
Ile	Met	Cys	Ala	Ala	Arg	Leu	Asn	Met	Tyr	Val	Gln	Ser	Leu	Ile	Met	
			260					265					270			
Leu	Leu	Thr	Lys	Arg	Asn	Val	Ser	Tyr	Arg	Ala	His	Glu	Leu	Leu	Gly	
		275					280					285				
Cys	Leu	Val	Phe	Ser	Ile	Trp	Tyr	Pro	Leu	Leu	Val	Ser	Cys	Leu	Pro	
	290					295					300					
Asn	Trp	Gly	Glu	Arg	Ile	Met	Phe	Val	Ile	Ala	Ser	Leu	Ser	Val	Thr	
305					310					315					320	
Gly	Met	Gln	Gln	Val	Gln	Phe	Ser	Leu	Asn	His	Phe	Ser	Ser	Ser	Val	
				325					330					335		
Tyr	Val	Gly	Lys	Pro	Lys	Gly	Asn	Asn	Trp	Phe	Glu	Lys	Gln	Thr	Asp	
			340					345					350			
Gly	Thr	Leu	Asp	Ile	Ser	Cys	Pro	Pro	Trp	Met	Asp	Trp	Phe	His	Gly	
		355					360					365				



Gly Leu Gln Phe Gln Ile Glu His His Leu Phe Pro Lys Met Pro Arg  
 370 375 380

Cys Asn Leu Arg Lys Ile Ser Pro Tyr Val Ile Glu Leu Cys Lys Lys  
 385 390 395 400

His Asn Leu Pro Tyr Asn Tyr Ala Ser Phe Ser Lys Ala Asn Glu Met  
 405 410 415

Thr Leu Arg Thr Leu Arg Asn Thr Ala Leu Gln Ala Arg Asp Ile Thr  
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Lys Pro Leu Pro Lys Asn Leu Val Trp Glu Ala Leu His Thr His Gly  
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<210> 3

<211> 1192

<212> DNA

<213> Physcomitrella patens

<220>

<221> CDS

<222> (58) .. (930)

<223> D6-elongase

<400> 3

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 Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser  
 1 5 10 15

cag ggc gtg aat gca ttg ctg ggt agt ttt ggg gtg gag ttg acg gat 153  
 Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp  
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acg ccc act acc aaa ggc ttg ccc ctc gtt gac agt ccc aca ccc atc 201  
 Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile  
 35 40 45

gtc ctc ggt gtt tct gta tac ttg act att gtc att gga ggg ctt ttg 249  
 Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu  
 50 55 60

tgg ata aag gcc agg gat ctg aaa ccg cgc gcc tcg gag cca ttt ttg 297  
 Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu  
 65 70 75 80

ctc caa gct ttg gtg ctt gtg cac aac ctg ttc tgt ttt gcg ctc agt 345  
 Leu Gln Ala Leu Val Leu Val His Asn Leu Phe Cys Phe Ala Leu Ser  
 85 90 95

ctg tat atg tgc gtg ggc atc gct tat cag gct att acc tgg cgg tac 393  
 Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln Ala Ile Thr Trp Arg Tyr  
 100 105 110

tct ctc tgg ggc aat gca tac aat cct aaa cat aaa gag atg gcg att	441
Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys His Lys Glu Met Ala Ile	
115 120 125	
ctg gta tac ttg ttc tac atg tct aag tac gtg gaa ttc atg gat acc	489
Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr Val Glu Phe Met Asp Thr	
130 135 140	
gtt atc atg ata ctg aag cgc agc acc agg caa ata agc ttc ctc cac	537
Val Ile Met Ile Leu Lys Arg Ser Thr Arg Gln Ile Ser Phe Leu His	
145 150 155 160	
gtt tat cat cat tct tca att tcc ctc att tgg tgg gct att gct cat	585
Val Tyr His His Ser Ser Ile Ser Leu Ile Trp Trp Ala Ile Ala His	
165 170 175	
cac gct cct ggc ggt gaa gca tat tgg tct gcg gct ctg aac tca gga	633
His Ala Pro Gly Gly Glu Ala Tyr Trp Ser Ala Ala Leu Asn Ser Gly	
180 185 190	
gtg cat gtt ctc atg tat gcg tat tac ttc ttg gct gcc tgc ctt cga	681
Val His Val Leu Met Tyr Ala Tyr Tyr Phe Leu Ala Ala Cys Leu Arg	
195 200 205	
agt agc cca aag tta aaa aat aag tac ctt ttt tgg ggc agg tac ttg	729
Ser Ser Pro Lys Leu Lys Asn Lys Tyr Leu Phe Trp Gly Arg Tyr Leu	
210 215 220	
aca caa ttc caa atg ttc cag ttt atg ctg aac tta gtg cag gct tac	777
Thr Gln Phe Gln Met Phe Gln Phe Met Leu Asn Leu Val Gln Ala Tyr	
225 230 235 240	
tac gac atg aaa acg aat gcg cca tat cca caa tgg ctg atc aag att	825
Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro Gln Trp Leu Ile Lys Ile	
245 250 255	
ttg ttc tac tac atg atc tcg ttg ctg ttt ctt ttc ggc aat ttt tac	873
Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe Leu Phe Gly Asn Phe Tyr	
260 265 270	
gta caa aaa tac atc aaa ccc tct gac gga aag caa aag gga gct aaa	921
Val Gln Lys Tyr Ile Lys Pro Ser Asp Gly Lys Gln Lys Gly Ala Lys	
275 280 285	
act gag tga gctgtatcaa gccatagaaa ctctattatg ttagaacctg	970
Thr Glu	
290	
aagttggtgc tttcttatct ccacttatct tttaagcagc atcagttttg aaatgatgtg	1030
tgggcgtggt ctgcaagtag tcatcaatat aatcggcctg agcacttcag atggattgtt	1090
agaacatgag taaaagcggg tattacgggtg tttattttgt accaaatcac cgcacgggtg	1150
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&lt;210&gt; 4

&lt;211&gt; 290

&lt;212&gt; PRT

<213> *Physcomitrella patens*

&lt;400&gt; 4

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Gln	Gly	Val	Asn	Ala	Leu	Leu	Gly	Ser	Phe	Gly	Val	Glu	Leu	Thr	Asp
			20					25					30		

Thr	Pro	Thr	Thr	Lys	Gly	Leu	Pro	Leu	Val	Asp	Ser	Pro	Thr	Pro	Ile
		35					40					45			

Val	Leu	Gly	Val	Ser	Val	Tyr	Leu	Thr	Ile	Val	Ile	Gly	Gly	Leu	Leu
	50					55					60				

Trp	Ile	Lys	Ala	Arg	Asp	Leu	Lys	Pro	Arg	Ala	Ser	Glu	Pro	Phe	Leu
65					70					75					80

Leu	Gln	Ala	Leu	Val	Leu	Val	His	Asn	Leu	Phe	Cys	Phe	Ala	Leu	Ser
				85					90					95	

Leu	Tyr	Met	Cys	Val	Gly	Ile	Ala	Tyr	Gln	Ala	Ile	Thr	Trp	Arg	Tyr
			100					105						110	

Ser	Leu	Trp	Gly	Asn	Ala	Tyr	Asn	Pro	Lys	His	Lys	Glu	Met	Ala	Ile
		115					120					125			

Leu	Val	Tyr	Leu	Phe	Tyr	Met	Ser	Lys	Tyr	Val	Glu	Phe	Met	Asp	Thr
	130					135					140				

Val	Ile	Met	Ile	Leu	Lys	Arg	Ser	Thr	Arg	Gln	Ile	Ser	Phe	Leu	His
145					150					155					160

Val	Tyr	His	His	Ser	Ser	Ile	Ser	Leu	Ile	Trp	Trp	Ala	Ile	Ala	His
				165					170					175	

His	Ala	Pro	Gly	Gly	Glu	Ala	Tyr	Trp	Ser	Ala	Ala	Leu	Asn	Ser	Gly
			180					185					190		

Val	His	Val	Leu	Met	Tyr	Ala	Tyr	Tyr	Phe	Leu	Ala	Ala	Cys	Leu	Arg
		195					200					205			

Ser	Ser	Pro	Lys	Leu	Lys	Asn	Lys	Tyr	Leu	Phe	Trp	Gly	Arg	Tyr	Leu
	210					215					220				

Thr	Gln	Phe	Gln	Met	Phe	Gln	Phe	Met	Leu	Asn	Leu	Val	Gln	Ala	Tyr
225				230						235					240

Tyr	Asp	Met	Lys	Thr	Asn	Ala	Pro	Tyr	Pro	Gln	Trp	Leu	Ile	Lys	Ile
				245					250					255	

Leu	Phe	Tyr	Tyr	Met	Ile	Ser	Leu	Leu	Phe	Leu	Phe	Gly	Asn	Phe	Tyr
			260					265					270		

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Thr Glu  
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 Leu Asp Arg Tyr Arg Ala Leu Ala Glu Leu Ala Ala Arg Tyr Ala Ser  
 5 10 15 20

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 Ser Ala Ala Phe Lys Trp Gln Val Thr Tyr Asp Ala Lys Asp Ser Phe  
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 Val Gly Pro Leu Gly Ile Arg Glu Pro Leu Gly Leu Leu Val Gly Ser  
 40 45 50

gtg gtc ctc tac ctg agc ctg ctg gcc gtg gtc tac gcg ctg cgg aac 246  
 Val Val Leu Tyr Leu Ser Leu Leu Ala Val Val Tyr Ala Leu Arg Asn  
 55 60 65

tac ctt ggc ggc ctc atg gcg ctc cgc agc gtg cat aac ctc ggg ctc 294  
 Tyr Leu Gly Gly Leu Met Ala Leu Arg Ser Val His Asn Leu Gly Leu  
 70 75 80

tgc ctc ttc tgc ggc gcc gtg tgg atc tac acg agc tac ctc atg atc 342  
 Cys Leu Phe Ser Gly Ala Val Trp Ile Tyr Thr Ser Tyr Leu Met Ile  
 85 90 95 100

cag gat ggg cac ttt cgc agc ctc gag gcg gca acg tgc gag ccg ctc 390  
 Gln Asp Gly His Phe Arg Ser Leu Glu Ala Ala Thr Cys Glu Pro Leu  
 105 110 115

aag cat ccg cac ttc cag ctc atc agc ttg ctc ttt gcg ctg tcc aag 438  
 Lys His Pro His Phe Gln Leu Ile Ser Leu Leu Phe Ala Leu Ser Lys  
 120 125 130

atc tgg gag tgg ttc gac acg gtg ctc ctc atc gtc aag ggc aac aag 486  
 Ile Trp Glu Trp Phe Asp Thr Val Leu Leu Ile Val Lys Gly Asn Lys

135	140	145	
ctc cgc ttc ctg cac gtc ttg cac cac gcc acg acc ttt tgg ctc tac			534
Leu Arg Phe Leu His Val Leu His His Ala Thr Thr Phe Trp Leu Tyr			
150	155	160	
gcc atc gac cac atc ttt ctc tcg tcc atc aag tac ggc gtc gcg gtc			582
Ala Ile Asp His Ile Phe Leu Ser Ser Ile Lys Tyr Gly Val Ala Val			
165	170	175	180
aat gct ttc atc cac acc gtc atg tac gcg cac tac ttc cgc cca ttc			630
Asn Ala Phe Ile His Thr Val Met Tyr Ala His Tyr Phe Arg Pro Phe			
185	190	195	
ccg aag ggc ttg cgc ccg ctt att acg cag ttg cag atc gtc cag ttc			678
Pro Lys Gly Leu Arg Pro Leu Ile Thr Gln Leu Gln Ile Val Gln Phe			
200	205	210	
att ttc agc atc ggc atc cat acc gcc att tac tgg cac tac gac tgc			726
Ile Phe Ser Ile Gly Ile His Thr Ala Ile Tyr Trp His Tyr Asp Cys			
215	220	225	
gag ccg ctc gtg cat acc cac ttt tgg gaa tac gtc acg ccc tac ctt			774
Glu Pro Leu Val His Thr His Phe Trp Glu Tyr Val Thr Pro Tyr Leu			
230	235	240	
ttc gtc gtg ccc ttc ctc atc ctc ttt ttc aat ttt tac ctg cag cag			822
Phe Val Val Pro Phe Leu Ile Leu Phe Phe Asn Phe Tyr Leu Gln Gln			
245	250	255	260
tac gtc ctc gcg ccc gca aaa acc aag aag gca tag ccacgtaaca			868
Tyr Val Leu Ala Pro Ala Lys Thr Lys Lys Ala			
265	270		
gtagaccagc agcgccgagg acgcgtgccg cgttatcgcg aagcacgaaa taaagaagat			928
catttgattc aacgaggcta cttgcggcca cgagaaaaaa aaaaaaaaaa aaaaaaaaaa			988
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Lys Asp Ser Phe Val Gly Pro Leu Gly Ile Arg Glu Pro Leu Gly Leu			
35	40	45	

Leu Val Gly Ser Val Val Leu Tyr Leu Ser Leu Leu Ala Val Val Tyr  
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 Ala Leu Arg Asn Tyr Leu Gly Gly Leu Met Ala Leu Arg Ser Val His  
 65 70 75 80  
 Asn Leu Gly Leu Cys Leu Phe Ser Gly Ala Val Trp Ile Tyr Thr Ser  
 85 90 95  
 Tyr Leu Met Ile Gln Asp Gly His Phe Arg Ser Leu Glu Ala Ala Thr  
 100 105 110  
 Cys Glu Pro Leu Lys His Pro His Phe Gln Leu Ile Ser Leu Leu Phe  
 115 120 125  
 Ala Leu Ser Lys Ile Trp Glu Trp Phe Asp Thr Val Leu Leu Ile Val  
 130 135 140  
 Lys Gly Asn Lys Leu Arg Phe Leu His Val Leu His His Ala Thr Thr  
 145 150 155 160  
 Phe Trp Leu Tyr Ala Ile Asp His Ile Phe Leu Ser Ser Ile Lys Tyr  
 165 170 175  
 Gly Val Ala Val Asn Ala Phe Ile His Thr Val Met Tyr Ala His Tyr  
 180 185 190  
 Phe Arg Pro Phe Pro Lys Gly Leu Arg Pro Leu Ile Thr Gln Leu Gln  
 195 200 205  
 Ile Val Gln Phe Ile Phe Ser Ile Gly Ile His Thr Ala Ile Tyr Trp  
 210 215 220  
 His Tyr Asp Cys Glu Pro Leu Val His Thr His Phe Trp Glu Tyr Val  
 225 230 235 240  
 Thr Pro Tyr Leu Phe Val Val Pro Phe Leu Ile Leu Phe Phe Asn Phe  
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 Tyr Leu Gln Gln Tyr Val Leu Ala Pro Ala Lys Thr Lys Lys Ala  
 260 265 270

<210> 7

<211> 2040

<212> DNA

<213> *Ceratodon purpureus*

<220>

<221> CDS

<222> (176) .. (1627)

<223> D6-desaturase

<400> 7

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tcagggtcga tcagggttatt ctgaaaaagg ctgcgtctgt gaggcagtttg caaaa atg																178
																Met 1
gcc ctc gtt acc gac ttt ctg aac ttt ctg ggc acg aca tgg agc aag																226
Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr Trp Ser Lys																
																5 10 15
tac agc gtg tac acc cat agc tat gct gga aac tat ggg cct act ttg																274
Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly Pro Thr Leu																
																20 25 30
aag cac gcc aaa aag gtt tct gct caa ggt aaa act gcg gga cag aca																322
Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala Gly Gln Thr																
																35 40 45
ctg aga cag aga tcg gtg cag gac aaa aag cca ggc act tac tct ctg																370
Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser Leu																
																50 55 60 65
gcc gat gtt gct tct cac gac agg cct gga gac tgc tgg atg atc gtc																418
Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile Val																
																70 75 80
aaa gag aag gtg tat gat att agc cgt ttt gcg gac gac cac cct gga																466
Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp His Pro Gly																
																85 90 95
ggg acg gta att agc acc tac ttt ggg cgg gat ggc aca gac gtt ttc																514
Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe																
																100 105 110
gca aca ttc cat cca cct gcc gca tgg aag caa ctc aat gac tac tac																562
Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn Asp Tyr Tyr																
																115 120 125
att gga gac ctt gct agg gaa gag ccc ctt gat gaa ttg ctt aaa gac																610
Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu Leu Lys Asp																
																130 135 140 145
tac aga gat atg aga gcc gag ttt gtt aga gaa ggg ctt ttc aag agt																658
Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu Phe Lys Ser																
																150 155 160
tcc aag gcc tgg ttc ctg ctt cag act ctg att aat gca gct ctc ttt																706
Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala Ala Leu Phe																
																165 170 175
gct gcg agc att gcg act atc tgt tac gac aag agt tac tgg gct att																754
Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr Trp Ala Ile																
																180 185 190
gtg ctg tca gcc agt ttg atg ggt ctc ttc gtc caa cag tgt gga tgg																802
Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln Cys Gly Trp																
																195 200 205

ctt gcc cat gat ttc ctt cat caa cag gtc ttt gag aac cgt acc gcg	850
Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn Arg Thr Ala	
210 215 220 225	
aac tcc ttc ttt ggc tat ttg ttc ggc aat tgc gtg ctt ggc ttt agt	898
Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu Gly Phe Ser	
230 235 240	
gta tca tgg tgg agg acg aag cac aac att cat cat act gct ccg aat	946
Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr Ala Pro Asn	
245 250 255	
gag tgc gac gaa cag tac aca cct cta gac gaa gac att gat act ctc	994
Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile Asp Thr Leu	
260 265 270	
ccc atc att gcc tgg agc aag gaa att ttg gcc acc gtt gag agc aag	1042
Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val Glu Ser Lys	
275 280 285	
aga att ttg cga gtg ctt caa tat cag cac tac atg att ctg cct cta	1090
Arg Ile Leu Arg Val Leu Gln Tyr Gln His Tyr Met Ile Leu Pro Leu	
290 295 300 305	
ttg ttc atg gcc cgg tac agt tgg act ttt gga agt ttg ctc ttc aca	1138
Leu Phe Met Ala Arg Tyr Ser Trp Thr Phe Gly Ser Leu Leu Phe Thr	
310 315 320	
ttc aat cct gat ttg agc acg acc aag gga ttg ata gag aag gga aca	1186
Phe Asn Pro Asp Leu Ser Thr Thr Lys Gly Leu Ile Glu Lys Gly Thr	
325 330 335	
gtt gct ttt cac tac gcc tgg ttc agt tgg gct gcg ttc cat att ttg	1234
Val Ala Phe His Tyr Ala Trp Phe Ser Trp Ala Ala Phe His Ile Leu	
340 345 350	
ccg ggt gtc gct aag cct ctt gcg tgg atg gta gca act gag ctt gtg	1282
Pro Gly Val Ala Lys Pro Leu Ala Trp Met Val Ala Thr Glu Leu Val	
355 360 365	
gcc ggt ttg ttg ttg gga ttc gtg ttt acg ttg agt cac aat gga aag	1330
Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His Asn Gly Lys	
370 375 380 385	
gag gtt tac aat gaa tcg aag gac ttc gtg aga gcc cag gtt att acc	1378
Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln Val Ile Thr	
390 395 400	
acc cgt aac acc aag cga ggc tgg ttc aac gat tgg ttc act ggg gga	1426
Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe Thr Gly Gly	
405 410 415	
ctc gac acc cag att gag cat cac ctg ttt cca aca atg ccc agg cac	1474
Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg His	
420 425 430	



aac tac ccc aag atc gca cct cag gtc gag gct ctt tgc aag aag cac 1522  
 Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys His  
 435 440 445

ggc ctc gag tac gat aat gtc tcc gtc gtt ggt gcc tct gtc gcg gtt 1570  
 Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala Val  
 450 455 460 465

gtg aag gcg ctc aag gaa att gct gat gaa gcg tca att cgg ctt cac 1618  
 Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu His  
 470 475 480

gct cac taa gaaatcgctg aactttgact attcattttt ttgcctggc 1667  
 Ala His

tacctcaaat gttcgggagc aggtgcttgg cagtgtgttc aaccggagcg cactgaaaat 1727

gtgcagaatc catttccaga aattaccatt cctagctaaa tcttcttttt accagggtcgg 1787

atatatgaaa cttttttgat gcaacaagta gcattcaatt gaagacattg ttcgagatat 1847

aattcgcagt gtttctattc agcgggcata cgtactagtc catatcggcg gttgccgaga 1907

gtttacatta ttagttggca caacgagtag atctagtgtgta aatttctatt tccgcatgta 1967

atattactct gaatatatac cgttatctat tttcctaaaa aaaaaaaaaa aaaaaaaaaa 2027

aaaaaaaaaa aaa 2040

<210> 8

<211> 483

<212> PRT

<213> *Ceratodon purpureus*

<400> 8

Met Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr Trp Ser  
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Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly Pro Thr  
 20 25 30

Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala Gly Gln  
 35 40 45

Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser  
 50 55 60

Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile  
 65 70 75 80

Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp His Pro  
 85 90 95

Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val  
 100 105 110

Phe	Ala	Thr	Phe	His	Pro	Pro	Ala	Ala	Trp	Lys	Gln	Leu	Asn	Asp	Tyr	115	120	125
Tyr	Ile	Gly	Asp	Leu	Ala	Arg	Glu	Glu	Pro	Leu	Asp	Glu	Leu	Leu	Lys	130	135	140
Asp	Tyr	Arg	Asp	Met	Arg	Ala	Glu	Phe	Val	Arg	Glu	Gly	Leu	Phe	Lys	145	150	155
Ser	Ser	Lys	Ala	Trp	Phe	Leu	Leu	Gln	Thr	Leu	Ile	Asn	Ala	Ala	Leu	165	170	175
Phe	Ala	Ala	Ser	Ile	Ala	Thr	Ile	Cys	Tyr	Asp	Lys	Ser	Tyr	Trp	Ala	180	185	190
Ile	Val	Leu	Ser	Ala	Ser	Leu	Met	Gly	Leu	Phe	Val	Gln	Gln	Cys	Gly	195	200	205
Trp	Leu	Ala	His	Asp	Phe	Leu	His	Gln	Gln	Val	Phe	Glu	Asn	Arg	Thr	210	215	220
Ala	Asn	Ser	Phe	Phe	Gly	Tyr	Leu	Phe	Gly	Asn	Cys	Val	Leu	Gly	Phe	225	230	235
Ser	Val	Ser	Trp	Trp	Arg	Thr	Lys	His	Asn	Ile	His	His	Thr	Ala	Pro	245	250	255
Asn	Glu	Cys	Asp	Glu	Gln	Tyr	Thr	Pro	Leu	Asp	Glu	Asp	Ile	Asp	Thr	260	265	270
Leu	Pro	Ile	Ile	Ala	Trp	Ser	Lys	Glu	Ile	Leu	Ala	Thr	Val	Glu	Ser	275	280	285
Lys	Arg	Ile	Leu	Arg	Val	Leu	Gln	Tyr	Gln	His	Tyr	Met	Ile	Leu	Pro	290	295	300
Leu	Leu	Phe	Met	Ala	Arg	Tyr	Ser	Trp	Thr	Phe	Gly	Ser	Leu	Leu	Phe	305	310	315
Thr	Phe	Asn	Pro	Asp	Leu	Ser	Thr	Thr	Lys	Gly	Leu	Ile	Glu	Lys	Gly	325	330	335
Thr	Val	Ala	Phe	His	Tyr	Ala	Trp	Phe	Ser	Trp	Ala	Ala	Phe	His	Ile	340	345	350
Leu	Pro	Gly	Val	Ala	Lys	Pro	Leu	Ala	Trp	Met	Val	Ala	Thr	Glu	Leu	355	360	365
Val	Ala	Gly	Leu	Leu	Leu	Gly	Phe	Val	Phe	Thr	Leu	Ser	His	Asn	Gly	370	375	380
Lys	Glu	Val	Tyr	Asn	Glu	Ser	Lys	Asp	Phe	Val	Arg	Ala	Gln	Val	Ile	385	390	395
Thr	Thr	Arg	Asn	Thr	Lys	Arg	Gly	Trp	Phe	Asn	Asp	Trp	Phe	Thr	Gly	405	410	415

Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg  
 420 425 430

His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys  
 435 440 445

His Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala  
 450 455 460

Val Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu  
 465 470 475 480

His Ala His

<210> 9

<211> 1467

<212> DNA

<213> Ceratodon purpureus

<220>

<221> CDS

<222> (10) .. (1461)

<223> D6-desaturase

<400> 9

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 Met Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr  
 1 5 10

tgg agc aag tac agc gtg tac acc cat agc tat gct gga aac tat ggg 99  
 Trp Ser Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly  
 15 20 25 30

cct act ttg aag cac gcc aaa aag gtt tct gct caa ggt aaa act gcg 147  
 Pro Thr Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala  
 35 40 45

gga cag aca ctg aga cag aga tcg gtg cag gac aaa aag cca ggc act 195  
 Gly Gln Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr  
 50 55 60

tac tct ctg gcc gat gtt gct tct cac gac agg cct gga gac tgc tgg 243  
 Tyr Ser Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp  
 65 70 75

atg atc gtc aaa gag aag gtg tat gat att agc cgt ttt gcg gac gac 291  
 Met Ile Val Lys Glu Lys Val Tyr Asp Ile Ser Arg Phe Ala Asp Asp  
 80 85 90

cac cct gga ggg acg gta att agc acc tac ttt ggg cgg gat ggc aca 339  
 His Pro Gly Gly Thr Val Ile Ser Thr Tyr Phe Gly Arg Asp Gly Thr  
 95 100 105 110

gac gtt ttc gca aca ttc cat cca cct gcc gca tgg aag caa ctc aat 387  
 Asp Val Phe Ala Thr Phe His Pro Pro Ala Ala Trp Lys Gln Leu Asn  
 115 120 125

gac tac tac att gga gac ctt gct agg gaa gag ccc ctt gat gaa ttg	435
Asp Tyr Tyr Ile Gly Asp Leu Ala Arg Glu Glu Pro Leu Asp Glu Leu	
130 135 140	
ctt aaa gac tac aga gat atg aga gcc gag ttt gtt aga gaa ggg ctt	483
Leu Lys Asp Tyr Arg Asp Met Arg Ala Glu Phe Val Arg Glu Gly Leu	
145 150 155	
ttc aag agt tcc aag gcc tgg ttc ctg ctt cag act ctg att aat gca	531
Phe Lys Ser Ser Lys Ala Trp Phe Leu Leu Gln Thr Leu Ile Asn Ala	
160 165 170	
gct ctc ttt gct gcg agc att gcg act atc tgt tac gac aag agt tac	579
Ala Leu Phe Ala Ala Ser Ile Ala Thr Ile Cys Tyr Asp Lys Ser Tyr	
175 180 185 190	
tgg gct att gtg ctg tca gcc agt ttg atg ggt ctc ttc gtc caa cag	627
Trp Ala Ile Val Leu Ser Ala Ser Leu Met Gly Leu Phe Val Gln Gln	
195 200 205	
tgt gga tgg ctt gcc cat gat ttc ctt cat caa cag gtc ttt gag aac	675
Cys Gly Trp Leu Ala His Asp Phe Leu His Gln Gln Val Phe Glu Asn	
210 215 220	
cgt acc gcg aac tcc ttc ttt ggc tat ttg ttc ggc aat tgc gtg ctt	723
Arg Thr Ala Asn Ser Phe Phe Gly Tyr Leu Phe Gly Asn Cys Val Leu	
225 230 235	
ggc ttt agt gta tca tgg tgg agg acg aag cac aac att cat cat act	771
Gly Phe Ser Val Ser Trp Trp Arg Thr Lys His Asn Ile His His Thr	
240 245 250	
gct ccg aat gag tgc gac gaa cag tac aca cct cta gac gaa gac att	819
Ala Pro Asn Glu Cys Asp Glu Gln Tyr Thr Pro Leu Asp Glu Asp Ile	
255 260 265 270	
gat act ctc ccc atc att gcc tgg agc aag gaa att ttg gcc acc gtt	867
Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Glu Ile Leu Ala Thr Val	
275 280 285	
gag agc aag aga att ttg cga gtg ctt caa tat cag cac tac atg att	915
Glu Ser Lys Arg Ile Leu Arg Val Leu Gln Tyr Gln His Tyr Met Ile	
290 295 300	
ctg cct cta ttg ttc atg gcc cgg tac agt tgg act ttt gga agt ttg	963
Leu Pro Leu Leu Phe Met Ala Arg Tyr Ser Trp Thr Phe Gly Ser Leu	
305 310 315	
ctc ttc aca ttc aat cct gat ttg agc acg acc aag gga ttg ata gag	1011
Leu Phe Thr Phe Asn Pro Asp Leu Ser Thr Thr Lys Gly Leu Ile Glu	
320 325 330	
aag gga aca gtt gct ttt cac tac gcc tgg ttc agt tgg gct gcg ttc	1059
Lys Gly Thr Val Ala Phe His Tyr Ala Trp Phe Ser Trp Ala Ala Phe	
335 340 345 350	

cat att ttg ccg ggt gtc gct aag cct ctt gcg tgg atg gta gca act	1107
His Ile Leu Pro Gly Val Ala Lys Pro Leu Ala Trp Met Val Ala Thr	
355 360 365	
gag ctt gtg gcc ggt ttg ttg ttg gga ttc gtg ttt acg ttg agt cac	1155
Glu Leu Val Ala Gly Leu Leu Leu Gly Phe Val Phe Thr Leu Ser His	
370 375 380	
aat gga aag gag gtt tac aat gaa tcg aag gac ttc gtg aga gcc cag	1203
Asn Gly Lys Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln	
385 390 395	
gtt att acc acc cgt aac acc aag cga ggc tgg ttc aac gat tgg ttc	1251
Val Ile Thr Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe	
400 405 410	
act ggg gga ctc gac acc cag att gag cat cac ctg ttt cca aca atg	1299
Thr Gly Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met	
415 420 425 430	
ccc agg cac aac tac ccc aag atc gca cct cag gtc gag gct ctt tgc	1347
Pro Arg His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys	
435 440 445	
aag aag cac ggc ctc gag tac gat aat gtc tcc gtc gtt ggt gcc tct	1395
Lys Lys His Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser	
450 455 460	
gtc gcg gtt gtg aag gcg ctc aag gaa att gct gat gaa gcg tca att	1443
Val Ala Val Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile	
465 470 475	
cgg ctt cac gct cac taa gtcgac	1467
Arg Leu His Ala His	
480	

&lt;210&gt; 10

&lt;211&gt; 483

&lt;212&gt; PRT

&lt;213&gt; Ceratodon purpureus

&lt;400&gt; 10

Met Ala Leu Val Thr Asp Phe Leu Asn Phe Leu Gly Thr Thr Trp Ser
1 5 10 15

Lys Tyr Ser Val Tyr Thr His Ser Tyr Ala Gly Asn Tyr Gly Pro Thr
20 25 30

Leu Lys His Ala Lys Lys Val Ser Ala Gln Gly Lys Thr Ala Gly Gln
35 40 45

Thr Leu Arg Gln Arg Ser Val Gln Asp Lys Lys Pro Gly Thr Tyr Ser
50 55 60

Leu Ala Asp Val Ala Ser His Asp Arg Pro Gly Asp Cys Trp Met Ile
65 70 75 80

Val	Lys	Glu	Lys	Val	Tyr	Asp	Ile	Ser	Arg	Phe	Ala	Asp	Asp	His	Pro	
				85					90					95		
Gly	Gly	Thr	Val	Ile	Ser	Thr	Tyr	Phe	Gly	Arg	Asp	Gly	Thr	Asp	Val	
			100					105					110			
Phe	Ala	Thr	Phe	His	Pro	Pro	Ala	Ala	Trp	Lys	Gln	Leu	Asn	Asp	Tyr	
		115					120					125				
Tyr	Ile	Gly	Asp	Leu	Ala	Arg	Glu	Glu	Pro	Leu	Asp	Glu	Leu	Leu	Lys	
	130					135					140					
Asp	Tyr	Arg	Asp	Met	Arg	Ala	Glu	Phe	Val	Arg	Glu	Gly	Leu	Phe	Lys	
145					150					155					160	
Ser	Ser	Lys	Ala	Trp	Phe	Leu	Leu	Gln	Thr	Leu	Ile	Asn	Ala	Ala	Leu	
			165						170						175	
Phe	Ala	Ala	Ser	Ile	Ala	Thr	Ile	Cys	Tyr	Asp	Lys	Ser	Tyr	Trp	Ala	
			180					185					190			
Ile	Val	Leu	Ser	Ala	Ser	Leu	Met	Gly	Leu	Phe	Val	Gln	Gln	Cys	Gly	
		195					200					205				
Trp	Leu	Ala	His	Asp	Phe	Leu	His	Gln	Gln	Val	Phe	Glu	Asn	Arg	Thr	
	210					215					220					
Ala	Asn	Ser	Phe	Phe	Gly	Tyr	Leu	Phe	Gly	Asn	Cys	Val	Leu	Gly	Phe	
225					230					235					240	
Ser	Val	Ser	Trp	Trp	Arg	Thr	Lys	His	Asn	Ile	His	His	Thr	Ala	Pro	
			245						250					255		
Asn	Glu	Cys	Asp	Glu	Gln	Tyr	Thr	Pro	Leu	Asp	Glu	Asp	Ile	Asp	Thr	
		260						265					270			
Leu	Pro	Ile	Ile	Ala	Trp	Ser	Lys	Glu	Ile	Leu	Ala	Thr	Val	Glu	Ser	
		275					280					285				
Lys	Arg	Ile	Leu	Arg	Val	Leu	Gln	Tyr	Gln	His	Tyr	Met	Ile	Leu	Pro	
	290					295					300					
Leu	Leu	Phe	Met	Ala	Arg	Tyr	Ser	Trp	Thr	Phe	Gly	Ser	Leu	Leu	Phe	
305				310						315					320	
Thr	Phe	Asn	Pro	Asp	Leu	Ser	Thr	Thr	Lys	Gly	Leu	Ile	Glu	Lys	Gly	
				325					330					335		
Thr	Val	Ala	Phe	His	Tyr	Ala	Trp	Phe	Ser	Trp	Ala	Ala	Phe	His	Ile	
			340					345					350			
Leu	Pro	Gly	Val	Ala	Lys	Pro	Leu	Ala	Trp	Met	Val	Ala	Thr	Glu	Leu	
		355					360					365				
Val	Ala	Gly	Leu	Leu	Leu	Gly	Phe	Val	Phe	Thr	Leu	Ser	His	Asn	Gly	
		370				375					380					

Lys Glu Val Tyr Asn Glu Ser Lys Asp Phe Val Arg Ala Gln Val Ile  
385 390 395 400

Thr Thr Arg Asn Thr Lys Arg Gly Trp Phe Asn Asp Trp Phe Thr Gly  
405 410 415

Gly Leu Asp Thr Gln Ile Glu His His Leu Phe Pro Thr Met Pro Arg  
420 425 430

His Asn Tyr Pro Lys Ile Ala Pro Gln Val Glu Ala Leu Cys Lys Lys  
435 440 445

His Gly Leu Glu Tyr Asp Asn Val Ser Val Val Gly Ala Ser Val Ala  
450 455 460

Val Val Lys Ala Leu Lys Glu Ile Ala Asp Glu Ala Ser Ile Arg Leu  
465 470 475 480

His Ala His

<210> 11

<211> 2160

<212> DNA

<213> Ceratodon purpureus

<220>

<221> CDS

<222> (159) .. (1721)

<223> D6-desaturase

<400> 11

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tttcgtgggt ttggcgttgg cattgcgcga gggcggacag tgggagtgcg ggaggtctgt 120

ttgtgcatga cgaggtgggt gtaatcttcg ccggcaga atg gtg tcc cag ggc ggc 176  
Met Val Ser Gln Gly Gly  
1 5

ggt ctc tcg cag ggt tcc att gaa gaa aac att gac gtt gag cac ttg 224  
Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn Ile Asp Val Glu His Leu  
10 15 20

gca acg atg ccc ctc gtc agt gac ttc cta aat gtc ctg gga acg act 272  
Ala Thr Met Pro Leu Val Ser Asp Phe Leu Asn Val Leu Gly Thr Thr  
25 30 35

ttg ggc cag tgg agt ctt tcc act aca ttc gct ttc aag agg ctc acg 320  
Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe Ala Phe Lys Arg Leu Thr  
40 45 50

act aag aaa cac agt tcg gac atc tcg gtg gag gca caa aaa gaa tcg 368  
Thr Lys Lys His Ser Ser Asp Ile Ser Val Glu Ala Gln Lys Glu Ser  
55 60 65 70

gtt gcg cgg ggg cca gtt gag aat att tct caa tcg gtt gcg cag ccc	416
Val Ala Arg Gly Pro Val Glu Asn Ile Ser Gln Ser Val Ala Gln Pro	
75 80 85	
atc agg cgg agg tgg gtg cag gat aaa aag ccg gtt act tac agc ctg	464
Ile Arg Arg Arg Trp Val Gln Asp Lys Lys Pro Val Thr Tyr Ser Leu	
90 95 100	
aag gat gta gct tcg cac gat atg ccc cag gac tgc tgg att ata atc	512
Lys Asp Val Ala Ser His Asp Met Pro Gln Asp Cys Trp Ile Ile Ile	
105 110 115	
aaa gag aag gtg tat gat gtg agc acc ttc gct gag cag cac cct gga	560
Lys Glu Lys Val Tyr Asp Val Ser Thr Phe Ala Glu Gln His Pro Gly	
120 125 130	
ggc acg gtt atc aac acc tac ttc gga cga gac gcc aca gat gtt ttc	608
Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg Asp Ala Thr Asp Val Phe	
135 140 145 150	
tct act ttc cac gca tcc acc tca tgg aag att ctt cag aat ttc tac	656
Ser Thr Phe His Ala Ser Thr Ser Trp Lys Ile Leu Gln Asn Phe Tyr	
155 160 165	
atc ggg aac ctt gtt agg gag gag ccg act ttg gag ctg ctg aag gag	704
Ile Gly Asn Leu Val Arg Glu Glu Pro Thr Leu Glu Leu Leu Lys Glu	
170 175 180	
tac aga gag ttg aga gcc ctt ttc ttg aga gaa cag ctt ttc aag agt	752
Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser	
185 190 195	
tcc aaa tcc tac tac ctt ttc aag act ctc ata aat gtt tcc att gtt	800
Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu Ile Asn Val Ser Ile Val	
200 205 210	
gcc aca agc att gcg ata atc agt ctg tac aag tct tac cgg gcg gtt	848
Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr Lys Ser Tyr Arg Ala Val	
215 220 225 230	
ctg tta tca gcc agt ttg atg ggc ttg ttt att caa cag tgc gga tgg	896
Leu Leu Ser Ala Ser Leu Met Gly Leu Phe Ile Gln Gln Cys Gly Trp	
235 240 245	
ttg tct cac gat ttt cta cac cat cag gta ttt gag aca cgc tgg ctc	944
Leu Ser His Asp Phe Leu His His Gln Val Phe Glu Thr Arg Trp Leu	
250 255 260	
aat gac gtt gtt ggc tat gtg gtc ggc aac gtt gtt ctg gga ttc agt	992
Asn Asp Val Val Gly Tyr Val Val Gly Asn Val Val Leu Gly Phe Ser	
265 270 275	
gtc tcg tgg tgg aag acc aag cac aac ctg cat cat gct gct ccg aat	1040
Val Ser Trp Trp Lys Thr Lys His Asn Leu His His Ala Ala Pro Asn	
280 285 290	
gaa tgc gac caa aag tac aca ccg att gat gag gat att gat act ctc	1088





520

tgttcatatg tgatcgaggg gaaaaggtcc catgctctga tctattcttc tgtagccaat 1821  
 atttttcaat tgaaaggagg ttcctcactt atcttccatc tatcgttgca catcctgcat 1881  
 cagagtttagc gttggagtaa tgtaagcac ttgtagatta tgcccacat tgccacattt 1941  
 ctgttcgggtt acaatcgttt gattccatgc taccctccgt gttcatctcg ttgttataag 2001  
 caagcttgaa aaaacatgct acgagattgg cagacgttgt cttggcagct gtagaggttg 2061  
 gttccattca ttgtgtagta cagaactctc tcgtccctgt ttctctacat tacttgttac 2121  
 atagtgcatt tcattcacag caaaaaaaaaa aaaaaaaaaa 2160

&lt;210&gt; 12

&lt;211&gt; 520

&lt;212&gt; PRT

<213> *Ceratodon purpureus*

&lt;400&gt; 12

Met	Val	Ser	Gln	Gly	Gly	Gly	Leu	Ser	Gln	Gly	Ser	Ile	Glu	Glu	Asn
1				5					10					15	
Ile	Asp	Val	Glu	His	Leu	Ala	Thr	Met	Pro	Leu	Val	Ser	Asp	Phe	Leu
			20					25					30		
Asn	Val	Leu	Gly	Thr	Thr	Leu	Gly	Gln	Trp	Ser	Leu	Ser	Thr	Thr	Phe
		35					40					45			
Ala	Phe	Lys	Arg	Leu	Thr	Thr	Lys	Lys	His	Ser	Ser	Asp	Ile	Ser	Val
	50					55					60				
Glu	Ala	Gln	Lys	Glu	Ser	Val	Ala	Arg	Gly	Pro	Val	Glu	Asn	Ile	Ser
65					70					75					80
Gln	Ser	Val	Ala	Gln	Pro	Ile	Arg	Arg	Arg	Trp	Val	Gln	Asp	Lys	Lys
				85					90					95	
Pro	Val	Thr	Tyr	Ser	Leu	Lys	Asp	Val	Ala	Ser	His	Asp	Met	Pro	Gln
			100					105					110		
Asp	Cys	Trp	Ile	Ile	Ile	Lys	Glu	Lys	Val	Tyr	Asp	Val	Ser	Thr	Phe
		115					120					125			
Ala	Glu	Gln	His	Pro	Gly	Gly	Thr	Val	Ile	Asn	Thr	Tyr	Phe	Gly	Arg
	130					135					140				
Asp	Ala	Thr	Asp	Val	Phe	Ser	Thr	Phe	His	Ala	Ser	Thr	Ser	Trp	Lys
145					150					155					160
Ile	Leu	Gln	Asn	Phe	Tyr	Ile	Gly	Asn	Leu	Val	Arg	Glu	Glu	Pro	Thr
			165						170					175	
Leu	Glu	Leu	Leu	Lys	Glu	Tyr	Arg	Glu	Leu	Arg	Ala	Leu	Phe	Leu	Arg

180						185						190					
Glu	Gln	Leu	Phe	Lys	Ser	Ser	Lys	Ser	Tyr	Tyr	Leu	Phe	Lys	Thr	Leu		
195						200						205					
Ile	Asn	Val	Ser	Ile	Val	Ala	Thr	Ser	Ile	Ala	Ile	Ile	Ser	Leu	Tyr		
210						215						220					
Lys	Ser	Tyr	Arg	Ala	Val	Leu	Leu	Ser	Ala	Ser	Leu	Met	Gly	Leu	Phe		
225						230						235					
Ile	Gln	Gln	Cys	Gly	Trp	Leu	Ser	His	Asp	Phe	Leu	His	His	Gln	Val		
245						250						255					
Phe	Glu	Thr	Arg	Trp	Leu	Asn	Asp	Val	Val	Gly	Tyr	Val	Val	Gly	Asn		
260						265						270					
Val	Val	Leu	Gly	Phe	Ser	Val	Ser	Trp	Trp	Lys	Thr	Lys	His	Asn	Leu		
275						280						285					
His	His	Ala	Ala	Pro	Asn	Glu	Cys	Asp	Gln	Lys	Tyr	Thr	Pro	Ile	Asp		
290						295						300					
Glu	Asp	Ile	Asp	Thr	Leu	Pro	Ile	Ile	Ala	Trp	Ser	Lys	Asp	Leu	Leu		
305						310						315					
Ala	Thr	Val	Glu	Ser	Lys	Thr	Met	Leu	Arg	Val	Leu	Gln	Tyr	Gln	His		
325						330						335					
Leu	Phe	Phe	Leu	Val	Leu	Leu	Thr	Phe	Ala	Arg	Ala	Ser	Trp	Leu	Phe		
340						345						350					
Trp	Ser	Ala	Ala	Phe	Thr	Leu	Arg	Pro	Glu	Leu	Thr	Leu	Gly	Glu	Lys		
355						360						365					
Leu	Leu	Glu	Arg	Gly	Thr	Met	Ala	Leu	His	Tyr	Ile	Trp	Phe	Asn	Ser		
370						375						380					
Val	Ala	Phe	Tyr	Leu	Leu	Pro	Gly	Trp	Lys	Pro	Val	Val	Trp	Met	Val		
385						390						395					
Val	Ser	Glu	Leu	Met	Ser	Gly	Phe	Leu	Leu	Gly	Tyr	Val	Phe	Val	Leu		
405						410						415					
Ser	His	Asn	Gly	Met	Glu	Val	Tyr	Asn	Thr	Ser	Lys	Asp	Phe	Val	Asn		
420						425						430					
Ala	Gln	Ile	Ala	Ser	Thr	Arg	Asp	Ile	Lys	Ala	Gly	Val	Phe	Asn	Asp		
435						440						445					
Trp	Phe	Thr	Gly	Gly	Leu	Asn	Arg	Gln	Ile	Glu	His	His	Leu	Phe	Pro		
450						455						460					
Thr	Met	Pro	Arg	His	Asn	Leu	Asn	Lys	Ile	Ser	Pro	His	Val	Glu	Thr		
465						470						475					
Leu	Cys	Lys	Lys	His	Gly	Leu	Val	Tyr	Glu	Asp	Val	Ser	Met	Ala	Ser		

485

490

495

Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala  
                   500                  505                  510

Ser His Gln Gln Leu Ala Ala Ser  
           515                  520

&lt;210&gt; 13

&lt;211&gt; 1434

&lt;212&gt; DNA

<213> *Phaeodactylum tricornutum*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (1434)

&lt;223&gt; D6-desaturase

&lt;400&gt; 13

atg ggc aaa gga ggg gac gct cgg gcc tcg aag ggc tca acg gcg gct 48  
 Met Gly Lys Gly Gly Asp Ala Arg Ala Ser Lys Gly Ser Thr Ala Ala  
   1                  5                  10                  15

cgc aag atc agt tgg cag gaa gtc aag acc cac gcg tct ccg gag gac 96  
 Arg Lys Ile Ser Trp Gln Glu Val Lys Thr His Ala Ser Pro Glu Asp  
                   20                  25                  30

gcc tgg atc att cac tcc aat aag gtc tac gac gtg tcc aac tgg cac 144  
 Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn Trp His  
                   35                  40                  45

gaa cat ccc gga ggc gcc gtc att ttc acg cac gcc ggt gac gac atg 192  
 Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met  
                   50                  55                  60

acg gac att ttc gct gcc ttt cac gca ccc gga tcg cag tcg ctc atg 240  
 Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met  
   65                  70                  75                  80

aag aag ttc tac att ggc gaa ttg ctc ccg gaa acc acc ggc aag gag 288  
 Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu  
                   85                  90                  95

ccg cag caa atc gcc ttt gaa aag ggc tac cgc gat ctg cgc tcc aaa 336  
 Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys  
                   100                  105                  110

ctc atc atg atg ggc atg ttc aag tcc aac aag tgg ttc tac gtc tac 384  
 Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr  
                   115                  120                  125

aag tgc ctc agc aac atg gcc att tgg gcc gcc gcc tgt gct ctc gtc 432  
 Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val  
                   130                  135                  140

ttt tac tcg gac cgc ttc tgg gta cac ctg gcc agc gcc gtc atg ctg 480

Phe 145	Tyr	Ser	Asp	Arg	Phe 150	Trp	Val	His	Leu	Ala 155	Ser	Ala	Val	Met	Leu 160	
gga Gly	aca Thr	ttc Phe	ttt Phe	cag Gln	cag Gln	tcg Ser	gga Gly	tgg Trp	ttg Leu	gca Ala	cac His	gac Asp	ttt Phe	ctg Leu	cac His	528
				165					170					175		
cac His	cag Gln	gtc Val	ttc Phe	acc Thr	aag Lys	cgc Arg	aag Lys	cac His	ggg Gly	gat Asp	ctc Leu	gga Gly	gga Gly	ctc Leu	ttt Phe	576
			180					185					190			
tgg Trp	ggg Gly	aac Asn	ctc Leu	atg Met	cag Gln	ggg Gly	tac Tyr	tcc Ser	gta Val	cag Gln	tgg Trp	tgg Trp	aaa Lys	aac Asn	aag Lys	624
		195					200					205				
cac His	aac Asn	gga Gly	cac His	cac His	gcc Ala	gtc Val	ccc Pro	aac Asn	ctc Leu	cac His	tgc Cys	tcc Ser	tcc Ser	gca Ala	gtc Val	672
	210					215					220					
gcg Ala	caa Gln	gat Asp	ggg Gly	gac Asp	ccg Pro	gac Asp	atc Ile	gat Asp	acc Thr	atg Met	ccc Pro	ctt Leu	ctc Leu	gcc Ala	tgg Trp	720
225					230					235					240	
tcc Ser	gtc Val	cag Gln	caa Gln	gcc Ala	cag Gln	tct Ser	tac Tyr	cgg Arg	gaa Glu	ctc Leu	caa Gln	gcc Ala	gac Asp	gga Gly	aag Lys	768
				245					250					255		
gat Asp	tcg Ser	ggg Gly	ttg Leu	gtc Val	aag Lys	ttc Phe	atg Met	atc Ile	cgt Arg	aac Asn	caa Gln	tcc Ser	tac Tyr	ttt Phe	tac Tyr	816
			260				265						270			
ttt Phe	ccc Pro	atc Ile	ttg Leu	ttg Leu	ctc Leu	gcc Ala	cgc Arg	ctg Leu	tcg Ser	tgg Trp	ttg Leu	aac Asn	gag Glu	tcc Ser	ttc Phe	864
	275						280					285				
aag Lys	tgc Cys	gcc Ala	ttt Phe	ggg Gly	ctt Leu	gga Gly	gct Ala	gcg Ala	tcg Ser	gag Glu	aac Asn	gct Ala	gct Ala	ctc Leu	gaa Glu	912
	290					295					300					
ctc Leu	aag Lys	gcc Ala	aag Lys	ggg Gly	ctt Leu	cag Gln	tac Tyr	ccc Pro	ctt Leu	ttg Leu	gaa Glu	aag Lys	gct Ala	ggc Gly	atc Ile	960
305					310					315					320	
ctg Leu	ctg Leu	cac His	tac Tyr	gct Ala	tgg Trp	atg Met	ctt Leu	aca Thr	gtt Val	tcg Ser	tcc Ser	ggc Gly	ttt Phe	gga Gly	cgc Arg	1008
				325					330					335		
ttc Phe	tcg Ser	ttc Phe	gcg Ala	tac Tyr	acc Thr	gca Ala	ttt Phe	tac Tyr	ttt Phe	cta Leu	acc Thr	gcg Ala	acc Thr	gcg Ala	tcc Ser	1056
			340				345					350				
tgt Cys	gga Gly	ttc Phe	ttg Leu	ctc Leu	gcc Ala	att Ile	gtc Val	ttt Phe	ggc Gly	ctc Leu	ggc Gly	cac His	aac Asn	ggc Gly	atg Met	1104
		355					360					365				
gcc Ala	acc Thr	tac Tyr	aat Asn	gcc Ala	gac Asp	gcc Ala	cgt Arg	ccg Pro	gac Asp	ttc Phe	tgg Trp	aag Lys	ctc Leu	caa Gln	gtc Val	1152

370	375	380	
acc acg act cgc aac gtc acg ggc gga cac ggt ttc ccc caa gcc ttt			1200
Thr Thr Thr Arg Asn Val Thr Gly Gly His Gly Phe Pro Gln Ala Phe			
385	390	395	400
gtc gac tgg ttc tgt ggt ggc ctc cag tac caa gtc gac cac cac tta			1248
Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp His His Leu			
405	410		415
ttc ccc agc ctg ccc cga cac aat ctg gcc aag aca cac gca ctg gtc			1296
Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val			
420	425		430
gaa tcg ttc tgc aag gag tgg ggt gtc cag tac cac gaa gcc gac ctt			1344
Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu			
435	440		445
gtg gac ggg acc atg gaa gtc ttg cac cat ttg ggc agc gtg gcc ggc			1392
Val Asp Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly			
450	455		460
gaa ttc gtc gtg gat ttt gta cgc gat gga ccc gcc atg taa			1434
Glu Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met			
465	470		475

&lt;210&gt; 14

&lt;211&gt; 477

&lt;212&gt; PRT

<213> *Phaeodactylum tricornutum*

&lt;400&gt; 14

Met Gly Lys Gly Gly Asp Ala Arg Ala Ser Lys Gly Ser Thr Ala Ala	
1 5 10 15	
Arg Lys Ile Ser Trp Gln Glu Val Lys Thr His Ala Ser Pro Glu Asp	
20 25 30	
Ala Trp Ile Ile His Ser Asn Lys Val Tyr Asp Val Ser Asn Trp His	
35 40 45	
Glu His Pro Gly Gly Ala Val Ile Phe Thr His Ala Gly Asp Asp Met	
50 55 60	
Thr Asp Ile Phe Ala Ala Phe His Ala Pro Gly Ser Gln Ser Leu Met	
65 70 75 80	
Lys Lys Phe Tyr Ile Gly Glu Leu Leu Pro Glu Thr Thr Gly Lys Glu	
85 90 95	
Pro Gln Gln Ile Ala Phe Glu Lys Gly Tyr Arg Asp Leu Arg Ser Lys	
100 105 110	
Leu Ile Met Met Gly Met Phe Lys Ser Asn Lys Trp Phe Tyr Val Tyr	
115 120 125	

Lys Cys Leu Ser Asn Met Ala Ile Trp Ala Ala Ala Cys Ala Leu Val  
 130 135 140  
 Phe Tyr Ser Asp Arg Phe Trp Val His Leu Ala Ser Ala Val Met Leu  
 145 150 155 160  
 Gly Thr Phe Phe Gln Gln Ser Gly Trp Leu Ala His Asp Phe Leu His  
 165 170 175  
 His Gln Val Phe Thr Lys Arg Lys His Gly Asp Leu Gly Gly Leu Phe  
 180 185 190  
 Trp Gly Asn Leu Met Gln Gly Tyr Ser Val Gln Trp Trp Lys Asn Lys  
 195 200 205  
 His Asn Gly His His Ala Val Pro Asn Leu His Cys Ser Ser Ala Val  
 210 215 220  
 Ala Gln Asp Gly Asp Pro Asp Ile Asp Thr Met Pro Leu Leu Ala Trp  
 225 230 235 240  
 Ser Val Gln Gln Ala Gln Ser Tyr Arg Glu Leu Gln Ala Asp Gly Lys  
 245 250 255  
 Asp Ser Gly Leu Val Lys Phe Met Ile Arg Asn Gln Ser Tyr Phe Tyr  
 260 265 270  
 Phe Pro Ile Leu Leu Leu Ala Arg Leu Ser Trp Leu Asn Glu Ser Phe  
 275 280 285  
 Lys Cys Ala Phe Gly Leu Gly Ala Ala Ser Glu Asn Ala Ala Leu Glu  
 290 295 300  
 Leu Lys Ala Lys Gly Leu Gln Tyr Pro Leu Leu Glu Lys Ala Gly Ile  
 305 310 315 320  
 Leu Leu His Tyr Ala Trp Met Leu Thr Val Ser Ser Gly Phe Gly Arg  
 325 330 335  
 Phe Ser Phe Ala Tyr Thr Ala Phe Tyr Phe Leu Thr Ala Thr Ala Ser  
 340 345 350  
 Cys Gly Phe Leu Leu Ala Ile Val Phe Gly Leu Gly His Asn Gly Met  
 355 360 365  
 Ala Thr Tyr Asn Ala Asp Ala Arg Pro Asp Phe Trp Lys Leu Gln Val  
 370 375 380  
 Thr Thr Thr Arg Asn Val Thr Gly Gly His Gly Phe Pro Gln Ala Phe  
 385 390 395 400  
 Val Asp Trp Phe Cys Gly Gly Leu Gln Tyr Gln Val Asp His His Leu  
 405 410 415  
 Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Thr His Ala Leu Val  
 420 425 430

Glu Ser Phe Cys Lys Glu Trp Gly Val Gln Tyr His Glu Ala Asp Leu  
 435 440 445

Val Asp Gly Thr Met Glu Val Leu His His Leu Gly Ser Val Ala Gly  
 450 455 460

Glu Phe Val Val Asp Phe Val Arg Asp Gly Pro Ala Met  
 465 470 475

<210> 15

<211> 1563

<212> DNA

<213> *Ceratodon purpureus*

<220>

<221> CDS

<222> (1) .. (1563)

<223> D6-desaturase

<400> 15

atg gtg tcc cag ggc ggc ggt ctc tcg cag ggt tcc att gaa gaa aac 48  
 Met Val Ser Gln Gly Gly Gly Leu Ser Gln Gly Ser Ile Glu Glu Asn  
 1 5 10 15

att gac gtt gag cac ttg gca acg atg ccc ctc gtc agt gac ttc cta 96  
 Ile Asp Val Glu His Leu Ala Thr Met Pro Leu Val Ser Asp Phe Leu  
 20 25 30

aat gtc ctg gga acg act ttg ggc cag tgg agt ctt tcc act aca ttc 144  
 Asn Val Leu Gly Thr Thr Leu Gly Gln Trp Ser Leu Ser Thr Thr Phe  
 35 40 45

gct ttc aag agg ctc acg act aag aaa cac agt tcg gac atc tcg gtg 192  
 Ala Phe Lys Arg Leu Thr Thr Lys Lys His Ser Ser Asp Ile Ser Val  
 50 55 60

gag gca caa aaa gaa tcg gtt gcg cgg ggg cca gtt gag aat att tct 240  
 Glu Ala Gln Lys Glu Ser Val Ala Arg Gly Pro Val Glu Asn Ile Ser  
 65 70 75 80

caa tcg gtt gcg cag ccc atc agg cgg agg tgg gtg cag gat aaa aag 288  
 Gln Ser Val Ala Gln Pro Ile Arg Arg Arg Trp Val Gln Asp Lys Lys  
 85 90 95

ccg gtt act tac agc ctg aag gat gta gct tcg cac gat atg ccc cag 336  
 Pro Val Thr Tyr Ser Leu Lys Asp Val Ala Ser His Asp Met Pro Gln  
 100 105 110

gac tgc tgg att ata atc aaa gag aag gtg tat gat gtg agc acc ttc 384  
 Asp Cys Trp Ile Ile Ile Lys Glu Lys Val Tyr Asp Val Ser Thr Phe  
 115 120 125

gct gag cag cac cct gga ggc acg gtt atc aac acc tac ttc gga cga 432  
 Ala Glu Gln His Pro Gly Gly Thr Val Ile Asn Thr Tyr Phe Gly Arg  
 130 135 140



gac gcc aca gat gtt ttc tct act ttc cac gca tcc acc tca tgg aag	480
Asp Ala Thr Asp Val Phe Ser Thr Phe His Ala Ser Thr Ser Trp Lys	
145 150 155 160	
att ctt cag aat ttc tac atc ggg aac ctt gtt agg gag gag ccg act	528
Ile Leu Gln Asn Phe Tyr Ile Gly Asn Leu Val Arg Glu Glu Pro Thr	
165 170 175	
ttg gag ctg ctg aag gag tac aga gag ttg aga gcc ctt ttc ttg aga	576
Leu Glu Leu Leu Lys Glu Tyr Arg Glu Leu Arg Ala Leu Phe Leu Arg	
180 185 190	
gaa cag ctt ttc aag agt tcc aaa tcc tac tac ctt ttc aag act ctc	624
Glu Gln Leu Phe Lys Ser Ser Lys Ser Tyr Tyr Leu Phe Lys Thr Leu	
195 200 205	
ata aat gtt tcc att gtt gcc aca agc att gcg ata atc agt ctg tac	672
Ile Asn Val Ser Ile Val Ala Thr Ser Ile Ala Ile Ile Ser Leu Tyr	
210 215 220	
aag tct tac cgg gcg gtt ctg tta tca gcc agt ttg atg ggc ttg ttt	720
Lys Ser Tyr Arg Ala Val Leu Leu Ser Ala Ser Leu Met Gly Leu Phe	
225 230 235 240	
att caa cag tgc gga tgg ttg tct cac gat ttt cta cac cat cag gta	768
Ile Gln Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val	
245 250 255	
ttt gag aca cgc tgg ctc aat gac gtt gtt ggc tat gtg gtc ggc aac	816
Phe Glu Thr Arg Trp Leu Asn Asp Val Val Gly Tyr Val Val Gly Asn	
260 265 270	
gtt gtt ctg gga ttc agt gtc tcg tgg tgg aag acc aag cac aac ctg	864
Val Val Leu Gly Phe Ser Val Ser Trp Trp Lys Thr Lys His Asn Leu	
275 280 285	
cat cat gct gct ccg aat gaa tgc gac caa aag tac aca ccg att gat	912
His His Ala Ala Pro Asn Glu Cys Asp Gln Lys Tyr Thr Pro Ile Asp	
290 295 300	
gag gat att gat act ctc ccc atc att gct tgg agt aaa gat ctc ttg	960
Glu Asp Ile Asp Thr Leu Pro Ile Ile Ala Trp Ser Lys Asp Leu Leu	
305 310 315 320	
gcc act gtt gag agc aag acc atg ttg cga gtt ctt cag tac cag cac	1008
Ala Thr Val Glu Ser Lys Thr Met Leu Arg Val Leu Gln Tyr Gln His	
325 330 335	
cta ttc ttt ttg gtt ctt ttg acg ttt gcc cgg gcg agt tgg cta ttt	1056
Leu Phe Phe Leu Val Leu Leu Thr Phe Ala Arg Ala Ser Trp Leu Phe	
340 345 350	
ttg agc gcg gcc ttc act ctc agg ccc gag ttg acc ctt ggc gag aag	1104
Trp Ser Ala Ala Phe Thr Leu Arg Pro Glu Leu Thr Leu Gly Glu Lys	
355 360 365	
ctt ttg gag agg gga acg atg gct ttg cac tac att tgg ttt aat agt	1152

Leu	Leu	Glu	Arg	Gly	Thr	Met	Ala	Leu	His	Tyr	Ile	Trp	Phe	Asn	Ser		
370						375					380						
gtt	gcg	ttt	tat	ctg	ctc	ccc	gga	tgg	aaa	cca	gtt	gta	tgg	atg	gtg	1200	
Val	Ala	Phe	Tyr	Leu	Leu	Pro	Gly	Trp	Lys	Pro	Val	Val	Trp	Met	Val		
385					390					395					400		
gtc	agc	gag	ctc	atg	tct	ggg	ttc	ctg	ctg	gga	tac	gta	ttt	gta	ctc	1248	
Val	Ser	Glu	Leu	Met	Ser	Gly	Phe	Leu	Leu	Gly	Tyr	Val	Phe	Val	Leu		
				405					410					415			
agt	cac	aat	gga	atg	gag	gtg	tac	aat	acg	tca	aag	gac	ttc	gtg	aat	1296	
Ser	His	Asn	Gly	Met	Glu	Val	Tyr	Asn	Thr	Ser	Lys	Asp	Phe	Val	Asn		
			420					425					430				
gcc	cag	att	gca	tcg	act	cgc	gac	atc	aaa	gca	ggg	gtg	ttt	aat	gat	1344	
Ala	Gln	Ile	Ala	Ser	Thr	Arg	Asp	Ile	Lys	Ala	Gly	Val	Phe	Asn	Asp		
			435				440					445					
tgg	ttc	acc	gga	ggg	ctc	aac	aga	cag	att	gag	cat	cat	cta	ttt	cca	1392	
Trp	Phe	Thr	Gly	Gly	Leu	Asn	Arg	Gln	Ile	Glu	His	His	Leu	Phe	Pro		
	450					455					460						
acg	atg	ccc	agg	cac	aac	ctt	aat	aaa	att	tct	cct	cac	gtg	gag	act	1440	
Thr	Met	Pro	Arg	His	Asn	Leu	Asn	Lys	Ile	Ser	Pro	His	Val	Glu	Thr		
465					470					475					480		
ttg	tgc	aag	aag	cat	gga	ctg	gtc	tac	gaa	gac	gtg	agc	atg	gct	tcg	1488	
Leu	Cys	Lys	Lys	His	Gly	Leu	Val	Tyr	Glu	Asp	Val	Ser	Met	Ala	Ser		
				485				490						495			
ggc	act	tac	cgg	gtt	ttg	aaa	aca	ctt	aag	gac	gtt	gcc	gat	gct	gct	1536	
Gly	Thr	Tyr	Arg	Val	Leu	Lys	Thr	Leu	Lys	Asp	Val	Ala	Asp	Ala	Ala		
			500					505					510				
tca	cac	cag	cag	ctt	gct	gcg	agt	tga								1563	
Ser	His	Gln	Gln	Leu	Ala	Ala	Ser										
		515					520										

&lt;210&gt; 16

&lt;211&gt; 520

&lt;212&gt; PRT

&lt;213&gt; Ceratodon purpureus

&lt;400&gt; 16

Met	Val	Ser	Gln	Gly	Gly	Gly	Leu	Ser	Gln	Gly	Ser	Ile	Glu	Glu	Asn		
1				5					10					15			
Ile	Asp	Val	Glu	His	Leu	Ala	Thr	Met	Pro	Leu	Val	Ser	Asp	Phe	Leu		
			20					25					30				
Asn	Val	Leu	Gly	Thr	Thr	Leu	Gly	Gln	Trp	Ser	Leu	Ser	Thr	Thr	Phe		
		35					40					45					
Ala	Phe	Lys	Arg	Leu	Thr	Thr	Lys	Lys	His	Ser	Ser	Asp	Ile	Ser	Val		
	50						55				60						

Glu	Ala	Gln	Lys	Glu	Ser	Val	Ala	Arg	Gly	Pro	Val	Glu	Asn	Ile	Ser	65	70	75	80
Gln	Ser	Val	Ala	Gln	Pro	Ile	Arg	Arg	Arg	Trp	Val	Gln	Asp	Lys	Lys	85	90	95	
Pro	Val	Thr	Tyr	Ser	Leu	Lys	Asp	Val	Ala	Ser	His	Asp	Met	Pro	Gln	100	105	110	
Asp	Cys	Trp	Ile	Ile	Ile	Lys	Glu	Lys	Val	Tyr	Asp	Val	Ser	Thr	Phe	115	120	125	
Ala	Glu	Gln	His	Pro	Gly	Gly	Thr	Val	Ile	Asn	Thr	Tyr	Phe	Gly	Arg	130	135	140	
Asp	Ala	Thr	Asp	Val	Phe	Ser	Thr	Phe	His	Ala	Ser	Thr	Ser	Trp	Lys	145	150	155	160
Ile	Leu	Gln	Asn	Phe	Tyr	Ile	Gly	Asn	Leu	Val	Arg	Glu	Glu	Pro	Thr	165	170	175	
Leu	Glu	Leu	Leu	Lys	Glu	Tyr	Arg	Glu	Leu	Arg	Ala	Leu	Phe	Leu	Arg	180	185	190	
Glu	Gln	Leu	Phe	Lys	Ser	Ser	Lys	Ser	Tyr	Tyr	Leu	Phe	Lys	Thr	Leu	195	200	205	
Ile	Asn	Val	Ser	Ile	Val	Ala	Thr	Ser	Ile	Ala	Ile	Ile	Ser	Leu	Tyr	210	215	220	
Lys	Ser	Tyr	Arg	Ala	Val	Leu	Leu	Ser	Ala	Ser	Leu	Met	Gly	Leu	Phe	225	230	235	240
Ile	Gln	Gln	Cys	Gly	Trp	Leu	Ser	His	Asp	Phe	Leu	His	His	Gln	Val	245	250	255	
Phe	Glu	Thr	Arg	Trp	Leu	Asn	Asp	Val	Val	Gly	Tyr	Val	Val	Gly	Asn	260	265	270	
Val	Val	Leu	Gly	Phe	Ser	Val	Ser	Trp	Trp	Lys	Thr	Lys	His	Asn	Leu	275	280	285	
His	His	Ala	Ala	Pro	Asn	Glu	Cys	Asp	Gln	Lys	Tyr	Thr	Pro	Ile	Asp	290	295	300	
Glu	Asp	Ile	Asp	Thr	Leu	Pro	Ile	Ile	Ala	Trp	Ser	Lys	Asp	Leu	Leu	305	310	315	320
Ala	Thr	Val	Glu	Ser	Lys	Thr	Met	Leu	Arg	Val	Leu	Gln	Tyr	Gln	His	325	330	335	
Leu	Phe	Phe	Leu	Val	Leu	Leu	Thr	Phe	Ala	Arg	Ala	Ser	Trp	Leu	Phe	340	345	350	
Trp	Ser	Ala	Ala	Phe	Thr	Leu	Arg	Pro	Glu	Leu	Thr	Leu	Gly	Glu	Lys	355	360	365	

Leu Leu Glu Arg Gly Thr Met Ala Leu His Tyr Ile Trp Phe Asn Ser  
 370 375 380  
 Val Ala Phe Tyr Leu Leu Pro Gly Trp Lys Pro Val Val Trp Met Val  
 385 390 395 400  
 Val Ser Glu Leu Met Ser Gly Phe Leu Leu Gly Tyr Val Phe Val Leu  
 405 410 415  
 Ser His Asn Gly Met Glu Val Tyr Asn Thr Ser Lys Asp Phe Val Asn  
 420 425 430  
 Ala Gln Ile Ala Ser Thr Arg Asp Ile Lys Ala Gly Val Phe Asn Asp  
 435 440 445  
 Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro  
 450 455 460  
 Thr Met Pro Arg His Asn Leu Asn Lys Ile Ser Pro His Val Glu Thr  
 465 470 475 480  
 Leu Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Met Ala Ser  
 485 490 495  
 Gly Thr Tyr Arg Val Leu Lys Thr Leu Lys Asp Val Ala Asp Ala Ala  
 500 505 510  
 Ser His Gln Gln Leu Ala Ala Ser  
 515 520

<210> 17  
 <211> 1578  
 <212> DNA  
 <213> *Physcomitrella patens*

<220>  
 <221> CDS  
 <222> (1) .. (1578)  
 <223> D6-desaturase

<400> 17  
 atg gta ttc gcg ggc ggt gga ctt cag cag ggc tct ctc gaa gaa aac 48  
 Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn  
 1 5 10 15  
 atc gac gtc gag cac att gcc agt atg tct ctc ttc agc gac ttc ttc 96  
 Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe  
 20 25 30  
 agt tat gtg tct tca act gtt ggt tcg tgg agc gta cac agt ata caa 144  
 Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln  
 35 40 45  
 cct ttg aag cgc ctg acg agt aag aag cgt gtt tcg gaa agc gct gcc 192  
 Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala

50	55	60	
gtg caa tgt ata tca gct gaa gtt cag aga aat tcg agt acc cag gga			240
Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly			
65	70	75	80
act gcg gag gca ctc gca gaa tca gtc gtg aag ccc acg aga cga agg			288
Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg			
	85	90	95
tca tct cag tgg aag aag tcg aca cac ccc cta tca gaa gta gca gta			336
Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val			
	100	105	110
cac aac aag cca agc gat tgc tgg att gtt gta aaa aac aag gtg tat			384
His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr			
	115	120	125
gat gtt tcc aat ttt gcg gac gag cat ccc gga gga tca gtt att agt			432
Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser			
	130	135	140
act tat ttt gga cga gac ggc aca gat gtt ttc tct agt ttt cat gca			480
Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala			
145	150	155	160
gct tct aca tgg aaa att ctt caa gac ttt tac att ggt gac gtg gag			528
Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu			
	165	170	175
agg gtg gag ccg act cca gag ctg ctg aaa gat ttc cga gaa atg aga			576
Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg			
	180	185	190
gct ctt ttc ctg agg gag caa ctt ttc aaa agt tcg aaa ttg tac tat			624
Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr			
	195	200	205
gtt atg aag ctg ctc acg aat gtt gct att ttt gct gcg agc att gca			672
Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala			
	210	215	220
ata ata tgt tgg agc aag act att tca gcg gtt ttg gct tca gct tgt			720
Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys			
225	230	235	240
atg atg gct ctg tgt ttc caa cag tgc gga tgg cta tcc cat gat ttt			768
Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe			
	245	250	255
ctc cac aat cag gtg ttt gag aca cgc tgg ctt aat gaa gtt gtc ggg			816
Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly			
	260	265	270
tat gtg atc ggc aac gcc gtt ctg ggg ttt agt aca ggg tgg tgg aag			864
Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys			
	275	280	285

gag aag cat aac ctt cat cat gct gct cca aat gaa tgc gat cag act	912
Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr	
290 295 300	
tac caa cca att gat gaa gat att gat act ctc ccc ctc att gcc tgg	960
Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp	
305 310 315 320	
agc aag gac ata ctg gcc aca gtt gag aat aag aca ttc ttg cga atc	1008
Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile	
325 330 335	
ctc caa tac cag cat ctg ttc ttc atg ggt ctg tta ttt ttc gcc cgt	1056
Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg	
340 345 350	
ggg agt tgg ctc ttt tgg agc tgg aga tat acc tct aca gca gtg ctc	1104
Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu	
355 360 365	
tca cct gtc gac agg ttg ttg gag aag gga act gtt ctg ttt cac tac	1152
Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr	
370 375 380	
ttt tgg ttc gtc ggg aca gcg tgc tat ctt ctc cct ggt tgg aag cca	1200
Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro	
385 390 395 400	
tta gta tgg atg gcg gtg act gag ctc atg tcc ggc atg ctg ctg ggc	1248
Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly	
405 410 415	
ttt gta ttt gta ctt agc cac aat ggg atg gag gtt tat aat tcg tct	1296
Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser	
420 425 430	
aaa gaa ttc gtg agt gca cag atc gta tcc aca cgg gat atc aaa gga	1344
Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly	
435 440 445	
aac ata ttc aac gac tgg ttc act ggt ggc ctt aac agg caa ata gag	1392
Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu	
450 455 460	
cat cat ctt ttc cca aca atg ccc agg cat aat tta aac aaa ata gca	1440
His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala	
465 470 475 480	
cct aga gtg gag gtg ttc tgt aag aaa cac ggt ctg gtg tac gaa gac	1488
Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp	
485 490 495	
gta tct att gct acc ggc act tgc aag gtt ttg aaa gca ttg aag gaa	1536
Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu	
500 505 510	

gtc gcg gag gct gcg gca gag cag cat gct acc acc agt taa  
 Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser  
           515                          520                          525

1578

&lt;210&gt; 18

&lt;211&gt; 525

&lt;212&gt; PRT

<213> *Physcomitrella patens*

&lt;400&gt; 18

Met Val Phe Ala Gly Gly Gly Leu Gln Gln Gly Ser Leu Glu Glu Asn  
       1                          5                          10                          15

Ile Asp Val Glu His Ile Ala Ser Met Ser Leu Phe Ser Asp Phe Phe  
           20                          25                          30

Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln  
           35                          40                          45

Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala  
       50                          55                          60

Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly  
       65                          70                          75                          80

Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg  
           85                          90                          95

Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val  
           100                          105                          110

His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr  
           115                          120                          125

Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser  
       130                          135                          140

Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala  
       145                          150                          155                          160

Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu  
           165                          170                          175

Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg  
           180                          185                          190

Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr  
       195                          200                          205

Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala  
       210                          215                          220

Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys  
       225                          230                          235                          240

Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe

245										250					255				
Leu	His	Asn	Gln	Val	Phe	Glu	Thr	Arg	Trp	Leu	Asn	Glu	Val	Val	Gly				
			260					265					270						
Tyr	Val	Ile	Gly	Asn	Ala	Val	Leu	Gly	Phe	Ser	Thr	Gly	Trp	Trp	Lys				
		275					280					285							
Glu	Lys	His	Asn	Leu	His	His	Ala	Ala	Pro	Asn	Glu	Cys	Asp	Gln	Thr				
	290					295					300								
Tyr	Gln	Pro	Ile	Asp	Glu	Asp	Ile	Asp	Thr	Leu	Pro	Leu	Ile	Ala	Trp				
305					310					315					320				
Ser	Lys	Asp	Ile	Leu	Ala	Thr	Val	Glu	Asn	Lys	Thr	Phe	Leu	Arg	Ile				
				325					330					335					
Leu	Gln	Tyr	Gln	His	Leu	Phe	Phe	Met	Gly	Leu	Leu	Phe	Phe	Ala	Arg				
			340					345					350						
Gly	Ser	Trp	Leu	Phe	Trp	Ser	Trp	Arg	Tyr	Thr	Ser	Thr	Ala	Val	Leu				
		355					360					365							
Ser	Pro	Val	Asp	Arg	Leu	Leu	Glu	Lys	Gly	Thr	Val	Leu	Phe	His	Tyr				
	370					375					380								
Phe	Trp	Phe	Val	Gly	Thr	Ala	Cys	Tyr	Leu	Leu	Pro	Gly	Trp	Lys	Pro				
385					390					395					400				
Leu	Val	Trp	Met	Ala	Val	Thr	Glu	Leu	Met	Ser	Gly	Met	Leu	Leu	Gly				
			405					410					415						
Phe	Val	Phe	Val	Leu	Ser	His	Asn	Gly	Met	Glu	Val	Tyr	Asn	Ser	Ser				
		420						425					430						
Lys	Glu	Phe	Val	Ser	Ala	Gln	Ile	Val	Ser	Thr	Arg	Asp	Ile	Lys	Gly				
		435					440					445							
Asn	Ile	Phe	Asn	Asp	Trp	Phe	Thr	Gly	Gly	Leu	Asn	Arg	Gln	Ile	Glu				
	450					455					460								
His	His	Leu	Phe	Pro	Thr	Met	Pro	Arg	His	Asn	Leu	Asn	Lys	Ile	Ala				
465					470						475				480				
Pro	Arg	Val	Glu	Val	Phe	Cys	Lys	Lys	His	Gly	Leu	Val	Tyr	Glu	Asp				
				485				490						495					
Val	Ser	Ile	Ala	Thr	Gly	Thr	Cys	Lys	Val	Leu	Lys	Ala	Leu	Lys	Glu				
		500						505					510						
Val	Ala	Glu	Ala	Ala	Ala	Glu	Gln	His	Ala	Thr	Thr	Ser							
		515					520					525							

&lt;210&gt; 19

&lt;211&gt; 837

&lt;212&gt; DNA



<213> *Phytophthora infestans*

<220>

<221> CDS

<222> (1) .. (837)

<223> D6-elongase

<400> 19

atg tcg act gag cta ctg cag agc tac tac gcg tgg gcc aac gcc acg	48
Met Ser Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr	
1 5 10 15	
 gag gcc aag ctg ctg gac tgg gtc gac cct gag ggc ggc tgg aag gtg	96
Glu Ala Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val	
20 25 30	
 cat cct atg gca gac tac ccc cta gcc aac ttc tcc agc gtc tac gcc	144
His Pro Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala	
35 40 45	
 atc tgc gtc gga tac ttg ctc ttc gta atc ttc ggc acg gcc ctg atg	192
Ile Cys Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met	
50 55 60	
 aaa atg gga gtc ccc gcc atc aag acc agt cca tta cag ttt gtg tac	240
Lys Met Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr	
65 70 75 80	
 aac ccc atc caa gtc att gcc tgc tct tat atg tgc gtg gag gcc gcc	288
Asn Pro Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala	
85 90 95	
 atc cag gcc tac cgc aac ggc tac acc gcc gcc ccg tgc aac gcc ttt	336
Ile Gln Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe	
100 105 110	
 aag tcc gac gac ccc gtc atg ggc aac gtt ctg tac ctc ttc tat ctc	384
Lys Ser Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu	
115 120 125	
 tcc aag atg ctc gac ctg tgc gac aca gtc ttc att atc cta gga aag	432
Ser Lys Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys	
130 135 140	
 aag tgg aaa cag ctt tcc atc ttg cac gtg tac cac cac ctt acc gtg	480
Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val	
145 150 155 160	
 ctt ttc gtc tac tat gtg acg ttc cgc gcc gct cag gac ggg gac tca	528
Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser	
165 170 175	
 tat gct acc atc gtg ctc aac ggc ttc gtg cac acc atc atg tac act	576
Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr	
180 185 190	
 tac tac ttc gtc agc gcc cac acg cgc aac att tgg tgg aag aag tac	624

Tyr Tyr Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr  
 195 200 205  
 ctc acg cgc att cag ctt atc cag ttc gtg acc atg aac gtg cag ggc 672  
 Leu Thr Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly  
 210 215 220  
 tac ctg acc tac tct cga cag tgc cca ggc atg cct cct aag gtg ccg 720  
 Tyr Leu Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro  
 225 230 235 240  
 ctc atg tac ctt gtg tac gtg cag tca ctc ttc tgg ctc ttc atg aat 768  
 Leu Met Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn  
 245 250 255  
 ttc tac att cgc gcg tac gtg ttc ggc ccc aag aaa ccg gcc gtg gag 816  
 Phe Tyr Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu  
 260 265 270  
 gaa tcg aag aag aag ttg taa 837  
 Glu Ser Lys Lys Lys Leu  
 275

<210> 20  
 <211> 278  
 <212> PRT  
 <213> *Phytophthora infestans*

<400> 20  
 Met Ser Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr  
 1 5 10 15  
 Glu Ala Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val  
 20 25 30  
 His Pro Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala  
 35 40 45  
 Ile Cys Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met  
 50 55 60  
 Lys Met Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr  
 65 70 75 80  
 Asn Pro Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala  
 85 90 95  
 Ile Gln Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe  
 100 105 110  
 Lys Ser Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu  
 115 120 125  
 Ser Lys Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys  
 130 135 140

Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val  
145 150 155 160

Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser  
165 170 175

Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr  
180 185 190

Tyr Tyr Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr  
195 200 205

Leu Thr Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly  
210 215 220

Tyr Leu Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro  
225 230 235 240

Leu Met Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn  
245 250 255

Phe Tyr Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu  
260 265 270

Glu Ser Lys Lys Lys Leu  
275

<210> 21

<211> 1410

<212> DNA

<213> *Phaeodactylum tricornutum*

<220>

<221> CDS

<222> (1) .. (1410)

<223> D5-desaturase

<400> 21

atg gct ccg gat gcg gat aag ctt cga caa cgc cag acg act gcg gta 48  
Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val  
1 5 10 15

gcg aag cac aat gct gct acc ata tcg acg cag gaa cgc ctt tgc agt 96  
Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser  
20 25 30

ctg tct tcg ctc aaa ggc gaa gaa gtc tgc atc gac gga atc atc tat 144  
Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr  
35 40 45

gac ctc caa tca ttc gat cat ccc ggg ggt gaa acg atc aaa atg ttt 192  
Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe  
50 55 60

ggt ggc aac gat gtc act gta cag tac aag atg att cac ccg tac cat 240  
Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His

65	70	75	80	
acc gag aag cat ttg gaa aag atg aag cgt gtc ggc aag gtg acg gat	288			
Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp				
85 90 95				
ttc gtc tgc gag tac aag ttc gat acc gaa ttt gaa cgc gaa atc aaa	336			
Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys				
100 105 110				
cga gaa gtc ttc aag att gtg cga cga ggc aag gat ttc ggt act ttg	384			
Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu				
115 120 125				
gga tgg ttc ttc cgt gcg ttt tgc tac att gcc att ttc ttc tac ctg	432			
Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu				
130 135 140				
cag tac cat tgg gtc acc acg gga acc tct tgg ctg ctg gcc gtg gcc	480			
Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala				
145 150 155 160				
tac gga atc tcc caa gcg atg att ggc atg aat gtc cag cac gat gcc	528			
Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala				
165 170 175				
aac cac ggg gcc acc tcc aag cgt ccc tgg gtc aac gac atg cta ggc	576			
Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly				
180 185 190				
ctc ggt gcg gat ttt att ggt ggt tcc aag tgg ctc tgg cag gaa caa	624			
Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln				
195 200 205				
cac tgg acc cac cac gct tac acc aat cac gcc gag atg gat ccc gat	672			
His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp				
210 215 220				
agc ttt ggt gcc gaa cca atg ctc cta ttc aac gac tat ccc ttg gat	720			
Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp				
225 230 235 240				
cat ccc gct cgt acc tgg cta cat cgc ttt caa gca ttc ttt tac atg	768			
His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met				
245 250 255				
ccc gtc ttg gct gga tac tgg ttg tcc gct gtc ttc aat cca caa att	816			
Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile				
260 265 270				
ctt gac ctc cag caa cgc ggc gca ctt tcc gtc ggt atc cgt ctc gac	864			
Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp				
275 280 285				
aac gct ttc att cac tcg cga cgc aag tat gcg gtt ttc tgg cgg gct	912			
Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala				
290 295 300				

gtg tac att gcg gtg aac gtg att gct ccg ttt tac aca aac tcc ggc	960
Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly	
305 310 315 320	
ctc gaa tgg tcc tgg cgt gtc ttt gga aac atc atg ctc atg ggt gtg	1008
Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val	
325 330 335	
gcg gaa tcg ctc gcg ctg gcg gtc ctg ttt tcg ttg tcg cac aat ttc	1056
Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe	
340 345 350	
gaa tcc gcg gat cgc gat ccg acc gcc cca ctg aaa aag acg gga gaa	1104
Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu	
355 360 365	
cca gtc gac tgg ttc aag aca cag gtc gaa act tcc tgc act tac ggt	1152
Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly	
370 375 380	
gga ttc ctt tcc ggt tgc ttc acg gga ggt ctc aac ttt cag gtt gaa	1200
Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu	
385 390 395 400	
cac cac ttg ttc cca cgc atg agc agc gct tgg tat ccc tac att gcc	1248
His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala	
405 410 415	
ccc aag gtc cgc gaa att tgc gcc aaa cac ggc gtc cac tac gcc tac	1296
Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr	
420 425 430	
tac ccg tgg atc cac caa aac ttt ctc tcc acc gtc cgc tac atg cac	1344
Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His	
435 440 445	
gcg gcc ggg acc ggt gcc aac tgg cgc cag atg gcc aga gaa aat ccc	1392
Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro	
450 455 460	
ttg acc gga cgg gcg taa	1410
Leu Thr Gly Arg Ala	
465 470	

&lt;210&gt; 22

&lt;211&gt; 469

&lt;212&gt; PRT

&lt;213&gt; Phaeodactylum tricornutum

&lt;400&gt; 22

Met Ala Pro Asp Ala Asp Lys Leu Arg Gln Arg Gln Thr Thr Ala Val
1 5 10 15

Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser
20 25 30

Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr  
                   35                                  40                                  45

Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe  
           50                                  55                                  60

Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His  
   65                                  70                                  75                                  80

Thr Glu Lys His Leu Glu Lys Met Lys Arg Val Gly Lys Val Thr Asp  
                                   85                                  90                                  95

Phe Val Cys Glu Tyr Lys Phe Asp Thr Glu Phe Glu Arg Glu Ile Lys  
                                   100                                  105                                  110

Arg Glu Val Phe Lys Ile Val Arg Arg Gly Lys Asp Phe Gly Thr Leu  
                                   115                                  120                                  125

Gly Trp Phe Phe Arg Ala Phe Cys Tyr Ile Ala Ile Phe Phe Tyr Leu  
                                   130                                  135                                  140

Gln Tyr His Trp Val Thr Thr Gly Thr Ser Trp Leu Leu Ala Val Ala  
   145                                  150                                  155                                  160

Tyr Gly Ile Ser Gln Ala Met Ile Gly Met Asn Val Gln His Asp Ala  
                                   165                                  170                                  175

Asn His Gly Ala Thr Ser Lys Arg Pro Trp Val Asn Asp Met Leu Gly  
                                   180                                  185                                  190

Leu Gly Ala Asp Phe Ile Gly Gly Ser Lys Trp Leu Trp Gln Glu Gln  
                                   195                                  200                                  205

His Trp Thr His His Ala Tyr Thr Asn His Ala Glu Met Asp Pro Asp  
                                   210                                  215                                  220

Ser Phe Gly Ala Glu Pro Met Leu Leu Phe Asn Asp Tyr Pro Leu Asp  
   225                                  230                                  235                                  240

His Pro Ala Arg Thr Trp Leu His Arg Phe Gln Ala Phe Phe Tyr Met  
                                   245                                  250                                  255

Pro Val Leu Ala Gly Tyr Trp Leu Ser Ala Val Phe Asn Pro Gln Ile  
                                   260                                  265                                  270

Leu Asp Leu Gln Gln Arg Gly Ala Leu Ser Val Gly Ile Arg Leu Asp  
                                   275                                  280                                  285

Asn Ala Phe Ile His Ser Arg Arg Lys Tyr Ala Val Phe Trp Arg Ala  
                                   290                                  295                                  300

Val Tyr Ile Ala Val Asn Val Ile Ala Pro Phe Tyr Thr Asn Ser Gly  
   305                                  310                                  315                                  320

Leu Glu Trp Ser Trp Arg Val Phe Gly Asn Ile Met Leu Met Gly Val  
                                   325                                  330                                  335

Ala Glu Ser Leu Ala Leu Ala Val Leu Phe Ser Leu Ser His Asn Phe  
 340 345 350

Glu Ser Ala Asp Arg Asp Pro Thr Ala Pro Leu Lys Lys Thr Gly Glu  
 355 360 365

Pro Val Asp Trp Phe Lys Thr Gln Val Glu Thr Ser Cys Thr Tyr Gly  
 370 375 380

Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu  
 385 390 395 400

His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala  
 405 410 415

Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr  
 420 425 430

Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His  
 435 440 445

Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro  
 450 455 460

Leu Thr Gly Arg Ala  
 465

<210> 23

<211> 1344

<212> DNA

<213> *Caenorhabditis elegans*

<220>

<221> CDS

<222> (1) .. (1344)

<223> D5-desaturase

<400> 23

atg gta tta cga gag caa gag cat gag cca ttc ttc att aaa att gat 48  
 Met Val Leu Arg Glu Gln Glu His Glu Pro Phe Phe Ile Lys Ile Asp  
 1 5 10 15

gga aaa tgg tgt caa att gac gat gct gtc ctg aga tca cat cca ggt 96  
 Gly Lys Trp Cys Gln Ile Asp Asp Ala Val Leu Arg Ser His Pro Gly  
 20 25 30

ggg agt gca att act acc tat aaa aat atg gat gcc act acc gta ttc 144  
 Gly Ser Ala Ile Thr Thr Tyr Lys Asn Met Asp Ala Thr Thr Val Phe  
 35 40 45

cac aca ttc cat act ggt tct aaa gaa gcg tat caa tgg ctg aca gaa 192  
 His Thr Phe His Thr Gly Ser Lys Glu Ala Tyr Gln Trp Leu Thr Glu  
 50 55 60

ttg aaa aaa gag tgc cct aca caa gaa cca gag atc cca gat att aag 240

Leu 65	Lys	Lys	Glu	Cys	Pro 70	Thr	Gln	Glu	Pro	Glu 75	Ile	Pro	Asp	Ile	Lys 80	
gat Asp	gac Asp	cca Pro	atc Ile	aaa Lys	gga Gly	att Ile	gat Asp	gat Asp	gtg Val	aac Asn	atg Met	gga Gly	act Thr	ttc Phe	aat Asn	288
				85					90					95		
att Ile	tct Ser	gag Glu	aaa Lys	cga Arg	tct Ser	gcc Ala	caa Gln	ata Ile	aat Asn	aaa Lys	agt Ser	ttc Phe	act Thr	gat Asp	cta Leu	336
			100					105					110			
cgt Arg	atg Met	cga Arg	gtt Val	cgt Arg	gca Ala	gaa Glu	gga Gly	ctt Leu	atg Met	gat Asp	gga Gly	tct Ser	cct Pro	ttg Leu	ttc Phe	384
		115					120					125				
tac Tyr	att Ile	aga Arg	aaa Lys	att Ile	ctt Leu	gaa Glu	aca Thr	atc Ile	ttc Phe	aca Thr	att Ile	ctt Leu	ttt Phe	gca Ala	ttc Phe	432
	130					135					140					
tac Tyr	ctt Leu	caa Gln	tac Tyr	cac His	aca Thr	tat Tyr	tat Tyr	ctt Leu	cca Pro	tca Ser	gct Ala	att Ile	cta Leu	atg Met	gga Gly	480
	145				150					155					160	
gtt Val	gcg Ala	tgg Trp	caa Gln	caa Gln	ttg Leu	gga Gly	tgg Trp	tta Leu	atc Ile	cat His	gaa Glu	ttc Phe	gca Ala	cat His	cat His	528
			165					170					175			
cag Gln	ttg Leu	ttc Phe	aaa Lys	aac Asn	aga Arg	tac Tyr	tac Tyr	aat Asn	gat Asp	ttg Leu	gcc Ala	agc Ser	tat Tyr	ttc Phe	gtt Val	576
			180					185					190			
gga Gly	aac Asn	ttt Phe	tta Leu	caa Gln	gga Gly	ttc Phe	tca Ser	tct Ser	ggt Gly	ggt Gly	tgg Trp	aaa Lys	gag Glu	cag Gln	cac His	624
		195					200					205				
aat Asn	gtg Val	cat His	cac His	gca Ala	gcc Ala	aca Thr	aat Asn	gtt Val	gtt Val	gga Gly	cga Arg	gac Asp	gga Gly	gat Asp	ctt Leu	672
	210					215					220					
gat Asp	tta Leu	gtc Val	cca Pro	ttc Phe	tat Tyr	gct Ala	aca Thr	gtg Val	gca Ala	gaa Glu	cat His	ctc Leu	aac Asn	aat Asn	tat Tyr	720
	225				230					235					240	
tct Ser	cag Gln	gat Asp	tca Ser	tgg Trp	gtt Val	atg Met	act Thr	cta Leu	ttc Phe	aga Arg	tgg Trp	caa Gln	cat His	gtt Val	cat His	768
				245					250					255		
tgg Trp	aca Thr	ttc Phe	atg Met	tta Leu	cca Pro	ttc Phe	ctc Leu	cgt Arg	ctc Leu	tcg Ser	tgg Trp	ctt Leu	ctt Leu	cag Gln	tca Ser	816
		260						265					270			
atc Ile	att Ile	ttt Phe	gtt Val	agt Ser	cag Gln	atg Met	cca Pro	act Thr	cat His	tat Tyr	tat Tyr	gac Asp	tat Tyr	tac Tyr	aga Arg	864
		275					280					285				
aat Asn	act Thr	gcg Ala	att Ile	tat Tyr	gaa Glu	cag Gln	gtt Val	ggt Gly	ctc Leu	tct Ser	ttg Leu	cac His	tgg Trp	gct Ala	tgg Trp	912



290	295	300	
tca ttg ggt caa ttg tat ttc cta ccc gat tgg tca act aga ata atg			960
Ser Leu Gly Gln Leu Tyr Phe Leu Pro Asp Trp Ser Thr Arg Ile Met			
305	310	315	320
ttc ttc ctt gtt tct cat ctt gtt gga ggt ttc ctg ctc tct cat gta			1008
Phe Phe Leu Val Ser His Leu Val Gly Gly Phe Leu Leu Ser His Val			
325	330		335
gtt act ttc aat cat tat tca gtg gag aag ttt gca ttg agc tcg aac			1056
Val Thr Phe Asn His Tyr Ser Val Glu Lys Phe Ala Leu Ser Ser Asn			
340	345		350
atc atg tca aat tac gct tgt ctt caa atc atg acc aca aga aat atg			1104
Ile Met Ser Asn Tyr Ala Cys Leu Gln Ile Met Thr Thr Arg Asn Met			
355	360		365
aga cct gga aga ttc att gac tgg ctt tgg gga ggt ctt aac tat cag			1152
Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln			
370	375		380
att gag cac cat ctt ttc cca acg atg cca cga cac aac ttg aac act			1200
Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr			
385	390	395	400
gtt atg cca ctt gtt aag gag ttt gca gca gca aat ggt tta cca tac			1248
Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr			
405	410		415
atg gtc gac gat tat ttc aca gga ttc tgg ctt gaa att gag caa ttc			1296
Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe			
420	425		430
cga aat att gca aat gtt gct gct aaa ttg act aaa aag att gcc tag			1344
Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala			
435	440		445

&lt;210&gt; 24

&lt;211&gt; 447

&lt;212&gt; PRT

&lt;213&gt; Caenorhabditis elegans

&lt;400&gt; 24

Met	Val	Leu	Arg	Glu	Gln	Glu	His	Glu	Pro	Phe	Phe	Ile	Lys	Ile	Asp
1				5					10					15	

Gly	Lys	Trp	Cys	Gln	Ile	Asp	Asp	Ala	Val	Leu	Arg	Ser	His	Pro	Gly
			20					25					30		

Gly	Ser	Ala	Ile	Thr	Thr	Tyr	Lys	Asn	Met	Asp	Ala	Thr	Thr	Val	Phe
		35					40					45			

His	Thr	Phe	His	Thr	Gly	Ser	Lys	Glu	Ala	Tyr	Gln	Trp	Leu	Thr	Glu
	50					55					60				

Leu	Lys	Lys	Glu	Cys	Pro	Thr	Gln	Glu	Pro	Glu	Ile	Pro	Asp	Ile	Lys	65	70	75	80
Asp	Asp	Pro	Ile	Lys	Gly	Ile	Asp	Asp	Val	Asn	Met	Gly	Thr	Phe	Asn	85	90	95	
Ile	Ser	Glu	Lys	Arg	Ser	Ala	Gln	Ile	Asn	Lys	Ser	Phe	Thr	Asp	Leu	100	105	110	
Arg	Met	Arg	Val	Arg	Ala	Glu	Gly	Leu	Met	Asp	Gly	Ser	Pro	Leu	Phe	115	120	125	
Tyr	Ile	Arg	Lys	Ile	Leu	Glu	Thr	Ile	Phe	Thr	Ile	Leu	Phe	Ala	Phe	130	135	140	
Tyr	Leu	Gln	Tyr	His	Thr	Tyr	Tyr	Leu	Pro	Ser	Ala	Ile	Leu	Met	Gly	145	150	155	160
Val	Ala	Trp	Gln	Gln	Leu	Gly	Trp	Leu	Ile	His	Glu	Phe	Ala	His	His	165	170	175	
Gln	Leu	Phe	Lys	Asn	Arg	Tyr	Tyr	Asn	Asp	Leu	Ala	Ser	Tyr	Phe	Val	180	185	190	
Gly	Asn	Phe	Leu	Gln	Gly	Phe	Ser	Ser	Gly	Gly	Trp	Lys	Glu	Gln	His	195	200	205	
Asn	Val	His	His	Ala	Ala	Thr	Asn	Val	Val	Gly	Arg	Asp	Gly	Asp	Leu	210	215	220	
Asp	Leu	Val	Pro	Phe	Tyr	Ala	Thr	Val	Ala	Glu	His	Leu	Asn	Asn	Tyr	225	230	235	240
Ser	Gln	Asp	Ser	Trp	Val	Met	Thr	Leu	Phe	Arg	Trp	Gln	His	Val	His	245	250	255	
Trp	Thr	Phe	Met	Leu	Pro	Phe	Leu	Arg	Leu	Ser	Trp	Leu	Leu	Gln	Ser	260	265	270	
Ile	Ile	Phe	Val	Ser	Gln	Met	Pro	Thr	His	Tyr	Tyr	Asp	Tyr	Tyr	Arg	275	280	285	
Asn	Thr	Ala	Ile	Tyr	Glu	Gln	Val	Gly	Leu	Ser	Leu	His	Trp	Ala	Trp	290	295	300	
Ser	Leu	Gly	Gln	Leu	Tyr	Phe	Leu	Pro	Asp	Trp	Ser	Thr	Arg	Ile	Met	305	310	315	320
Phe	Phe	Leu	Val	Ser	His	Leu	Val	Gly	Gly	Phe	Leu	Leu	Ser	His	Val	325	330	335	
Val	Thr	Phe	Asn	His	Tyr	Ser	Val	Glu	Lys	Phe	Ala	Leu	Ser	Ser	Asn	340	345	350	
Ile	Met	Ser	Asn	Tyr	Ala	Cys	Leu	Gln	Ile	Met	Thr	Thr	Arg	Asn	Met	355	360	365	

Arg Pro Gly Arg Phe Ile Asp Trp Leu Trp Gly Gly Leu Asn Tyr Gln  
 370 375 380  
 Ile Glu His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Thr  
 385 390 395 400  
 Val Met Pro Leu Val Lys Glu Phe Ala Ala Ala Asn Gly Leu Pro Tyr  
 405 410 415  
 Met Val Asp Asp Tyr Phe Thr Gly Phe Trp Leu Glu Ile Glu Gln Phe  
 420 425 430  
 Arg Asn Ile Ala Asn Val Ala Ala Lys Leu Thr Lys Lys Ile Ala  
 435 440 445

<210> 25  
 <211> 954  
 <212> DNA  
 <213> *Mortierella alpina*

<220>  
 <221> CDS  
 <222> (1) .. (954)  
 <223> D6-elongase

<400> 25  
 atg gcc gcc gca atc ttg gac aag gtc aac ttc ggc att gat cag ccc 48  
 Met Ala Ala Ala Ile Leu Asp Lys Val Asn Phe Gly Ile Asp Gln Pro  
 1 5 10 15  
 ttc gga atc aag ctc gac acc tac ttt gct cag gcc tat gaa ctc gtc 96  
 Phe Gly Ile Lys Leu Asp Thr Tyr Phe Ala Gln Ala Tyr Glu Leu Val  
 20 25 30  
 acc gga aag tcc atc gac tcc ttc gtc ttc cag gag ggc gtc acg cct 144  
 Thr Gly Lys Ser Ile Asp Ser Phe Val Phe Gln Glu Gly Val Thr Pro  
 35 40 45  
 ctc tcg acc cag aga gag gtc gcc atg tgg act atc act tac ttc gtc 192  
 Leu Ser Thr Gln Arg Glu Val Ala Met Trp Thr Ile Thr Tyr Phe Val  
 50 55 60  
 gtc atc ttt ggt ggt cgc cag atc atg aag agc cag gac gcc ttc aag 240  
 Val Ile Phe Gly Gly Arg Gln Ile Met Lys Ser Gln Asp Ala Phe Lys  
 65 70 75 80  
 ctc aag ccc ctc ttc atc ctc cac aac ttc ctc ctg acg atc gcg tcc 288  
 Leu Lys Pro Leu Phe Ile Leu His Asn Phe Leu Leu Thr Ile Ala Ser  
 85 90 95  
 gga tcg ctg ttg ctc ctg ttc atc gag aac ctg gtc ccc atc ctc gcc 336  
 Gly Ser Leu Leu Leu Leu Phe Ile Glu Asn Leu Val Pro Ile Leu Ala  
 100 105 110  
 aga aac gga ctt ttc tac gcc atc tgc gac gac ggt gcc tgg acc cag 384  
 Arg Asn Gly Leu Phe Tyr Ala Ile Cys Asp Asp Gly Ala Trp Thr Gln

115	120	125	
cgc ctc gag ctc ctc tac tac ctc aac tac ctg gtc aag tac tgg gag			432
Arg Leu Glu Leu Leu Tyr Tyr Leu Asn Tyr Leu Val Lys Tyr Trp Glu			
130	135	140	
ttg gcc gac acc gtc ttt ttg gtc ctc aag aag aag cct ctt gag ttc			480
Leu Ala Asp Thr Val Phe Leu Val Leu Lys Lys Lys Pro Leu Glu Phe			
145	150	155	160
ctg cac tac ttc cac cac tcg atg acc atg gtt ctc tgc ttt gtc cag			528
Leu His Tyr Phe His His Ser Met Thr Met Val Leu Cys Phe Val Gln			
	165	170	175
ctt gga gga tac act tca gtg tcc tgg gtc cct att acc ctc aac ttg			576
Leu Gly Gly Tyr Thr Ser Val Ser Trp Val Pro Ile Thr Leu Asn Leu			
	180	185	190
act gtc cac gtc ttc atg tac tac tac tac atg cgc tcc gct gcc ggt			624
Thr Val His Val Phe Met Tyr Tyr Tyr Tyr Met Arg Ser Ala Ala Gly			
	195	200	205
gtt cgc atc tgg tgg aag cag tac ttg acc act ctc cag atc gtc cag			672
Val Arg Ile Trp Trp Lys Gln Tyr Leu Thr Thr Leu Gln Ile Val Gln			
	210	215	220
ttc gtt ctt gac ctc gga ttc atc tac ttc tgc gcc tac acc tac ttc			720
Phe Val Leu Asp Leu Gly Phe Ile Tyr Phe Cys Ala Tyr Thr Tyr Phe			
225	230	235	240
gcc ttc acc tac ttc ccc tgg gct ccc aac gtc ggc aag tgc gcc ggt			768
Ala Phe Thr Tyr Phe Pro Trp Ala Pro Asn Val Gly Lys Cys Ala Gly			
	245	250	255
acc gag ggt gct gct ctc ttt ggc tgc gga ctc ctc tcc agc tat ctc			816
Thr Glu Gly Ala Ala Leu Phe Gly Cys Gly Leu Leu Ser Ser Tyr Leu			
	260	265	270
ttg ctc ttt atc aac ttc tac cgc att acc tac aat gcc aag gcc aag			864
Leu Leu Phe Ile Asn Phe Tyr Arg Ile Thr Tyr Asn Ala Lys Ala Lys			
	275	280	285
gca gcc aag gag cgt gga agc aac ttt acc ccc aag act gtc aag tcc			912
Ala Ala Lys Glu Arg Gly Ser Asn Phe Thr Pro Lys Thr Val Lys Ser			
	290	295	300
ggc gga tcg ccc aag aag ccc tcc aag agc aag cac atc taa			954
Gly Gly Ser Pro Lys Lys Pro Ser Lys Ser Lys His Ile			
305	310	315	

&lt;210&gt; 26

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Mortierella alpina

&lt;400&gt; 26

Met	Ala	Ala	Ala	Ile	Leu	Asp	Lys	Val	Asn	Phe	Gly	Ile	Asp	Gln	Pro	1	5	10	15
Phe	Gly	Ile	Lys	Leu	Asp	Thr	Tyr	Phe	Ala	Gln	Ala	Tyr	Glu	Leu	Val	20	25	30	
Thr	Gly	Lys	Ser	Ile	Asp	Ser	Phe	Val	Phe	Gln	Glu	Gly	Val	Thr	Pro	35	40	45	
Leu	Ser	Thr	Gln	Arg	Glu	Val	Ala	Met	Trp	Thr	Ile	Thr	Tyr	Phe	Val	50	55	60	
Val	Ile	Phe	Gly	Gly	Arg	Gln	Ile	Met	Lys	Ser	Gln	Asp	Ala	Phe	Lys	65	70	75	80
Leu	Lys	Pro	Leu	Phe	Ile	Leu	His	Asn	Phe	Leu	Leu	Thr	Ile	Ala	Ser	85	90	95	
Gly	Ser	Leu	Leu	Leu	Leu	Phe	Ile	Glu	Asn	Leu	Val	Pro	Ile	Leu	Ala	100	105	110	
Arg	Asn	Gly	Leu	Phe	Tyr	Ala	Ile	Cys	Asp	Asp	Gly	Ala	Trp	Thr	Gln	115	120	125	
Arg	Leu	Glu	Leu	Leu	Tyr	Tyr	Leu	Asn	Tyr	Leu	Val	Lys	Tyr	Trp	Glu	130	135	140	
Leu	Ala	Asp	Thr	Val	Phe	Leu	Val	Leu	Lys	Lys	Lys	Pro	Leu	Glu	Phe	145	150	155	160
Leu	His	Tyr	Phe	His	His	Ser	Met	Thr	Met	Val	Leu	Cys	Phe	Val	Gln	165	170	175	
Leu	Gly	Gly	Tyr	Thr	Ser	Val	Ser	Trp	Val	Pro	Ile	Thr	Leu	Asn	Leu	180	185	190	
Thr	Val	His	Val	Phe	Met	Tyr	Tyr	Tyr	Tyr	Met	Arg	Ser	Ala	Ala	Gly	195	200	205	
Val	Arg	Ile	Trp	Trp	Lys	Gln	Tyr	Leu	Thr	Thr	Leu	Gln	Ile	Val	Gln	210	215	220	
Phe	Val	Leu	Asp	Leu	Gly	Phe	Ile	Tyr	Phe	Cys	Ala	Tyr	Thr	Tyr	Phe	225	230	235	240
Ala	Phe	Thr	Tyr	Phe	Pro	Trp	Ala	Pro	Asn	Val	Gly	Lys	Cys	Ala	Gly	245	250	255	
Thr	Glu	Gly	Ala	Ala	Leu	Phe	Gly	Cys	Gly	Leu	Leu	Ser	Ser	Tyr	Leu	260	265	270	
Leu	Leu	Phe	Ile	Asn	Phe	Tyr	Arg	Ile	Thr	Tyr	Asn	Ala	Lys	Ala	Lys	275	280	285	
Ala	Ala	Lys	Glu	Arg	Gly	Ser	Asn	Phe	Thr	Pro	Lys	Thr	Val	Lys	Ser	290	295	300	

Gly Gly Ser Pro Lys Lys Pro Ser Lys Ser Lys His Ile  
 305 310 315

<210> 27

<211> 1320

<212> DNA

<213> Thraustochytrium

<220>

<221> CDS

<222> (1) .. (1320)

<223> D5-desaturase

<400> 27

atg ggc aag ggc agc gag ggc cgc agc gcg gcg cgc gag atg acg gcc	48
Met Gly Lys Gly Ser Glu Gly Arg Ser Ala Ala Arg Glu Met Thr Ala	
1 5 10 15	
 gag gcg aac ggc gac aag cgg aaa acg att ctg atc gag ggc gtc ctg	96
Glu Ala Asn Gly Asp Lys Arg Lys Thr Ile Leu Ile Glu Gly Val Leu	
20 25 30	
 tac gac gcg acg aac ttt aag cac ccg ggc ggt tcg atc atc aac ttc	144
Tyr Asp Ala Thr Asn Phe Lys His Pro Gly Gly Ser Ile Ile Asn Phe	
35 40 45	
 ttg acc gag ggc gag gcc ggc gtg gac gcg acg cag gcg tac cgc gag	192
Leu Thr Glu Gly Glu Ala Gly Val Asp Ala Thr Gln Ala Tyr Arg Glu	
50 55 60	
 ttt cat cag cgg tcc ggc aag gcc gac aag tac ctc aag tcg ctg ccg	240
Phe His Gln Arg Ser Gly Lys Ala Asp Lys Tyr Leu Lys Ser Leu Pro	
65 70 75 80	
 aag ctg gat gcg tcc aag gtg gag tcg cgg ttc tcg gcc aaa gag cag	288
Lys Leu Asp Ala Ser Lys Val Glu Ser Arg Phe Ser Ala Lys Glu Gln	
85 90 95	
 gcg cgg cgc gac gcc atg acg cgc gac tac gcg gcc ttt cgc gag gag	336
Ala Arg Arg Asp Ala Met Thr Arg Asp Tyr Ala Ala Phe Arg Glu Glu	
100 105 110	
 ctc gtc gcc gag ggg tac ttt gac ccg tcg atc ccg cac atg att tac	384
Leu Val Ala Glu Gly Tyr Phe Asp Pro Ser Ile Pro His Met Ile Tyr	
115 120 125	
 cgc gtc gtg gag atc gtg gcg ctc ttc gcg ctc tcg ttc tgg ctc atg	432
Arg Val Val Glu Ile Val Ala Leu Phe Ala Leu Ser Phe Trp Leu Met	
130 135 140	
 tcc aag gcc tcg ccc acc tcg ctc gtg ctg ggc gtg gtg atg aac ggc	480
Ser Lys Ala Ser Pro Thr Ser Leu Val Leu Gly Val Val Met Asn Gly	
145 150 155 160	
 att gcg cag ggc cgc tgc ggc tgg gtc atg cac gag atg ggc cac ggg	528
Ile Ala Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly	

165								170				175				
tgc	ttc	acg	ggc	gtc	atc	tgg	ctc	gac	gac	cgg	atg	tgc	gag	ttc	ttc	576
Ser	Phe	Thr	Gly	Val	Ile	Trp	Leu	Asp	Asp	Arg	Met	Cys	Glu	Phe	Phe	
			180				185						190			
tac	ggc	gtc	ggc	tgc	ggc	atg	agc	ggg	cac	tac	tgg	aag	aac	cag	cac	624
Tyr	Gly	Val	Gly	Cys	Gly	Met	Ser	Gly	His	Tyr	Trp	Lys	Asn	Gln	His	
			195				200						205			
agc	aag	cac	cac	gcc	gcg	ccc	aac	cgc	ctc	gag	cac	gat	gtc	gat	ctc	672
Ser	Lys	His	His	Ala	Ala	Pro	Asn	Arg	Leu	Glu	His	Asp	Val	Asp	Leu	
			210				215						220			
aac	acg	ctg	ccc	ctg	gtc	gcc	ttt	aac	gag	cgc	gtc	gtg	cgc	aag	gtc	720
Asn	Thr	Leu	Pro	Leu	Val	Ala	Phe	Asn	Glu	Arg	Val	Val	Arg	Lys	Val	
			225				230						235			240
aag	ccg	gga	tgc	ctg	ctg	gcg	ctc	tgg	ctg	cgc	gtg	cag	gcg	tac	ctc	768
Lys	Pro	Gly	Ser	Leu	Leu	Ala	Leu	Trp	Leu	Arg	Val	Gln	Ala	Tyr	Leu	
			245				250						255			
ttt	gcg	ccc	gtc	tgc	tgc	ctg	ctc	atc	ggc	ctt	ggc	tgg	acg	ctc	tac	816
Phe	Ala	Pro	Val	Ser	Cys	Leu	Leu	Ile	Gly	Leu	Gly	Trp	Thr	Leu	Tyr	
			260				265						270			
ctg	cac	ccg	cgc	tac	atg	ctg	cgc	acc	aag	cgg	cac	atg	gag	ttc	gtc	864
Leu	His	Pro	Arg	Tyr	Met	Leu	Arg	Thr	Lys	Arg	His	Met	Glu	Phe	Val	
			275				280						285			
tgg	atc	ttc	gcg	cgc	tac	att	ggc	tgg	ttc	tgc	ctc	atg	ggc	gct	ctc	912
Trp	Ile	Phe	Ala	Arg	Tyr	Ile	Gly	Trp	Phe	Ser	Leu	Met	Gly	Ala	Leu	
			290				295						300			
ggc	tac	tgc	ccg	ggc	acc	tgc	gtc	ggg	atg	tac	ctg	tgc	tgc	ttc	ggc	960
Gly	Tyr	Ser	Pro	Gly	Thr	Ser	Val	Gly	Met	Tyr	Leu	Cys	Ser	Phe	Gly	
			305				310						315			320
ctc	ggc	tgc	att	tac	att	ttc	ctg	cag	ttc	gcc	gtc	agc	cac	acg	cac	1008
Leu	Gly	Cys	Ile	Tyr	Ile	Phe	Leu	Gln	Phe	Ala	Val	Ser	His	Thr	His	
			325				330						335			
ctg	ccg	gtg	acc	aac	ccg	gag	gac	cag	ctg	cac	tgg	ctc	gag	tac	gcg	1056
Leu	Pro	Val	Thr	Asn	Pro	Glu	Asp	Gln	Leu	His	Trp	Leu	Glu	Tyr	Ala	
			340				345						350			
gcc	gac	cac	acg	gtg	aac	att	agc	acc	aag	tcc	tgg	ctc	gtc	acg	tgg	1104
Ala	Asp	His	Thr	Val	Asn	Ile	Ser	Thr	Lys	Ser	Trp	Leu	Val	Thr	Trp	
			355				360						365			
tgg	atg	tgc	aac	ctg	aac	ttt	cag	atc	gag	cac	cac	ctc	ttc	ccc	acg	1152
Trp	Met	Ser	Asn	Leu	Asn	Phe	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr	
			370				375						380			
gcg	ccg	cag	ttc	cgc	ttc	aag	gaa	atc	agt	cct	cgc	gtc	gag	gcc	ctc	1200
Ala	Pro	Gln	Phe	Arg	Phe	Lys	Glu	Ile	Ser	Pro	Arg	Val	Glu	Ala	Leu	
			385				390						395			400

ttc aag cgc cac aac ctc ccg tac tac gac ctg ccc tac acg agc gcg 1248  
 Phe Lys Arg His Asn Leu Pro Tyr Tyr Asp Leu Pro Tyr Thr Ser Ala  
                   405                  410                  415

gtc tcg acc acc ttt gcc aat ctt tat tcc gtc ggc cac tcg gtc ggc 1296  
 Val Ser Thr Thr Phe Ala Asn Leu Tyr Ser Val Gly His Ser Val Gly  
                   420                  425                  430

gcc gac acc aag aag cag gac tga 1320  
 Ala Asp Thr Lys Lys Gln Asp  
                   435                  440

<210> 28

<211> 439

<212> PRT

<213> Thraustochytrium

<400> 28

Met Gly Lys Gly Ser Glu Gly Arg Ser Ala Ala Arg Glu Met Thr Ala  
   1                  5                  10                  15

Glu Ala Asn Gly Asp Lys Arg Lys Thr Ile Leu Ile Glu Gly Val Leu  
                   20                  25                  30

Tyr Asp Ala Thr Asn Phe Lys His Pro Gly Gly Ser Ile Ile Asn Phe  
                   35                  40                  45

Leu Thr Glu Gly Glu Ala Gly Val Asp Ala Thr Gln Ala Tyr Arg Glu  
                   50                  55                  60

Phe His Gln Arg Ser Gly Lys Ala Asp Lys Tyr Leu Lys Ser Leu Pro  
   65                  70                  75                  80

Lys Leu Asp Ala Ser Lys Val Glu Ser Arg Phe Ser Ala Lys Glu Gln  
                   85                  90                  95

Ala Arg Arg Asp Ala Met Thr Arg Asp Tyr Ala Ala Phe Arg Glu Glu  
                   100                  105                  110

Leu Val Ala Glu Gly Tyr Phe Asp Pro Ser Ile Pro His Met Ile Tyr  
                   115                  120                  125

Arg Val Val Glu Ile Val Ala Leu Phe Ala Leu Ser Phe Trp Leu Met  
                   130                  135                  140

Ser Lys Ala Ser Pro Thr Ser Leu Val Leu Gly Val Val Met Asn Gly  
  145                  150                  155                  160

Ile Ala Gln Gly Arg Cys Gly Trp Val Met His Glu Met Gly His Gly  
                   165                  170                  175

Ser Phe Thr Gly Val Ile Trp Leu Asp Asp Arg Met Cys Glu Phe Phe  
                   180                  185                  190

Tyr Gly Val Gly Cys Gly Met Ser Gly His Tyr Trp Lys Asn Gln His



195					200					205						
Ser	Lys	His	His	Ala	Ala	Pro	Asn	Arg	Leu	Glu	His	Asp	Val	Asp	Leu	
210					215					220						
Asn	Thr	Leu	Pro	Leu	Val	Ala	Phe	Asn	Glu	Arg	Val	Val	Arg	Lys	Val	
225					230					235					240	
Lys	Pro	Gly	Ser	Leu	Leu	Ala	Leu	Trp	Leu	Arg	Val	Gln	Ala	Tyr	Leu	
245					250					255						
Phe	Ala	Pro	Val	Ser	Cys	Leu	Leu	Ile	Gly	Leu	Gly	Trp	Thr	Leu	Tyr	
260					265					270						
Leu	His	Pro	Arg	Tyr	Met	Leu	Arg	Thr	Lys	Arg	His	Met	Glu	Phe	Val	
275					280					285						
Trp	Ile	Phe	Ala	Arg	Tyr	Ile	Gly	Trp	Phe	Ser	Leu	Met	Gly	Ala	Leu	
290					295					300						
Gly	Tyr	Ser	Pro	Gly	Thr	Ser	Val	Gly	Met	Tyr	Leu	Cys	Ser	Phe	Gly	
305					310					315					320	
Leu	Gly	Cys	Ile	Tyr	Ile	Phe	Leu	Gln	Phe	Ala	Val	Ser	His	Thr	His	
325					330					335						
Leu	Pro	Val	Thr	Asn	Pro	Glu	Asp	Gln	Leu	His	Trp	Leu	Glu	Tyr	Ala	
340					345					350						
Ala	Asp	His	Thr	Val	Asn	Ile	Ser	Thr	Lys	Ser	Trp	Leu	Val	Thr	Trp	
355					360					365						
Trp	Met	Ser	Asn	Leu	Asn	Phe	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr	
370					375					380						
Ala	Pro	Gln	Phe	Arg	Phe	Lys	Glu	Ile	Ser	Pro	Arg	Val	Glu	Ala	Leu	
385					390					395					400	
Phe	Lys	Arg	His	Asn	Leu	Pro	Tyr	Tyr	Asp	Leu	Pro	Tyr	Thr	Ser	Ala	
405					410					415						
Val	Ser	Thr	Thr	Phe	Ala	Asn	Leu	Tyr	Ser	Val	Gly	His	Ser	Val	Gly	
420					425					430						
Ala	Asp	Thr	Lys	Lys	Gln	Asp										
435																

&lt;210&gt; 29

&lt;211&gt; 957

&lt;212&gt; DNA

&lt;213&gt; Mortierella alpina

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(957)

&lt;223&gt; D6-elongase

&lt;400&gt; 29

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Met Glu Ser Ile Ala Pro Phe Leu Pro Ser Lys Met Pro Gln Asp Leu	
1 5 10 15	
ttt atg gac ctt gcc acc gct atc ggt gtc cgg gcc gcg ccc tat gtc	96
Phe Met Asp Leu Ala Thr Ala Ile Gly Val Arg Ala Ala Pro Tyr Val	
20 25 30	
gat cct ctc gag gcc gcg ctg gtg gcc cag gcc gag aag tac atc ccc	144
Asp Pro Leu Glu Ala Ala Leu Val Ala Gln Ala Glu Lys Tyr Ile Pro	
35 40 45	
acg att gtc cat cac acg cgt ggg ttc ctg gtc gcg gtg gag tcg cct	192
Thr Ile Val His His Thr Arg Gly Phe Leu Val Ala Val Glu Ser Pro	
50 55 60	
ttg gcc cgt gag ctg ccg ttg atg aac ccg ttc cac gtg ctg ttg atc	240
Leu Ala Arg Glu Leu Pro Leu Met Asn Pro Phe His Val Leu Leu Ile	
65 70 75 80	
gtg ctc gct tat ttg gtc acg gtc ttt gtg ggc atg cag atc atg aag	288
Val Leu Ala Tyr Leu Val Thr Val Phe Val Gly Met Gln Ile Met Lys	
85 90 95	
aac ttt gag cgg ttc gag gtc aag acg ttt tcg ctc ctg cac aac ttt	336
Asn Phe Glu Arg Phe Glu Val Lys Thr Phe Ser Leu Leu His Asn Phe	
100 105 110	
tgt ctg gtc tcg atc agc gcc tac atg tgc ggt ggg atc ctg tac gag	384
Cys Leu Val Ser Ile Ser Ala Tyr Met Cys Gly Gly Ile Leu Tyr Glu	
115 120 125	
gct tat cag gcc aac tat gga ctg ttt gag aac gct gct gat cat acc	432
Ala Tyr Gln Ala Asn Tyr Gly Leu Phe Glu Asn Ala Ala Asp His Thr	
130 135 140	
ttc aag ggt ctt cct atg gcc aag atg atc tgg ctc ttc tac ttc tcc	480
Phe Lys Gly Leu Pro Met Ala Lys Met Ile Trp Leu Phe Tyr Phe Ser	
145 150 155 160	
aag atc atg gag ttt gtc gac acc atg atc atg gtc ctc aag aag aac	528
Lys Ile Met Glu Phe Val Asp Thr Met Ile Met Val Leu Lys Lys Asn	
165 170 175	
aac cgc cag atc tcc ttc ttg cac gtt tac cac cac agc tcc atc ttc	576
Asn Arg Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Phe	
180 185 190	
acc atc tgg tgg ttg gtc acc ttt gtt gca ccc aac ggt gaa gcc tac	624
Thr Ile Trp Trp Leu Val Thr Phe Val Ala Pro Asn Gly Glu Ala Tyr	
195 200 205	
ttc tct gct gcg ttg aac tcg ttc atc cat gtg atc atg tac ggc tac	672
Phe Ser Ala Ala Leu Asn Ser Phe Ile His Val Ile Met Tyr Gly Tyr	
210 215 220	

tac ttc ttg tcg gcc ttg ggc ttc aag cag gtg tcg ttc atc aag ttc 720  
 Tyr Phe Leu Ser Ala Leu Gly Phe Lys Gln Val Ser Phe Ile Lys Phe  
 225 230 235 240

tac atc acg cgc tcg cag atg aca cag ttc tgc atg atg tcg gtc cag 768  
 Tyr Ile Thr Arg Ser Gln Met Thr Gln Phe Cys Met Met Ser Val Gln  
 245 250 255

tct tcc tgg gac atg tac gcc atg aag gtc ctt ggc cgc ccc gga tac 816  
 Ser Ser Trp Asp Met Tyr Ala Met Lys Val Leu Gly Arg Pro Gly Tyr  
 260 265 270

ccc ttc ttc atc acg gct ctg ctt tgg ttc tac atg tgg acc atg ctc 864  
 Pro Phe Phe Ile Thr Ala Leu Leu Trp Phe Tyr Met Trp Thr Met Leu  
 275 280 285

ggc ctc ttc tac aac ttt tac aga aag aac gcc aag ttg gcc aag cag 912  
 Gly Leu Phe Tyr Asn Phe Tyr Arg Lys Asn Ala Lys Leu Ala Lys Gln  
 290 295 300

gcc aag gcc gac gct gcc aag gag aag gca agg aag ttg cag taa 957  
 Ala Lys Ala Asp Ala Ala Lys Glu Lys Ala Arg Lys Leu Gln  
 305 310 315

<210> 30

<211> 318

<212> PRT

<213> Mortierella alpina

<400> 30

Met Glu Ser Ile Ala Pro Phe Leu Pro Ser Lys Met Pro Gln Asp Leu  
 1 5 10 15

Phe Met Asp Leu Ala Thr Ala Ile Gly Val Arg Ala Ala Pro Tyr Val  
 20 25 30

Asp Pro Leu Glu Ala Ala Leu Val Ala Gln Ala Glu Lys Tyr Ile Pro  
 35 40 45

Thr Ile Val His His Thr Arg Gly Phe Leu Val Ala Val Glu Ser Pro  
 50 55 60

Leu Ala Arg Glu Leu Pro Leu Met Asn Pro Phe His Val Leu Leu Ile  
 65 70 75 80

Val Leu Ala Tyr Leu Val Thr Val Phe Val Gly Met Gln Ile Met Lys  
 85 90 95

Asn Phe Glu Arg Phe Glu Val Lys Thr Phe Ser Leu Leu His Asn Phe  
 100 105 110

Cys Leu Val Ser Ile Ser Ala Tyr Met Cys Gly Gly Ile Leu Tyr Glu  
 115 120 125

Ala Tyr Gln Ala Asn Tyr Gly Leu Phe Glu Asn Ala Ala Asp His Thr

130	135	140	
Phe Lys Gly Leu Pro Met Ala Lys Met Ile Trp Leu Phe Tyr Phe Ser			
145	150	155	160
Lys Ile Met Glu Phe Val Asp Thr Met Ile Met Val Leu Lys Lys Asn			
	165	170	175
Asn Arg Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Phe			
	180	185	190
Thr Ile Trp Trp Leu Val Thr Phe Val Ala Pro Asn Gly Glu Ala Tyr			
	195	200	205
Phe Ser Ala Ala Leu Asn Ser Phe Ile His Val Ile Met Tyr Gly Tyr			
	210	215	220
Tyr Phe Leu Ser Ala Leu Gly Phe Lys Gln Val Ser Phe Ile Lys Phe			
225	230	235	240
Tyr Ile Thr Arg Ser Gln Met Thr Gln Phe Cys Met Met Ser Val Gln			
	245	250	255
Ser Ser Trp Asp Met Tyr Ala Met Lys Val Leu Gly Arg Pro Gly Tyr			
	260	265	270
Pro Phe Phe Ile Thr Ala Leu Leu Trp Phe Tyr Met Trp Thr Met Leu			
	275	280	285
Gly Leu Phe Tyr Asn Phe Tyr Arg Lys Asn Ala Lys Leu Ala Lys Gln			
	290	295	300
Ala Lys Ala Asp Ala Ala Lys Glu Lys Ala Arg Lys Leu Gln			
305	310	315	

<210> 31  
 <211> 1374  
 <212> DNA  
 <213> Mortierella alpina

<220>  
 <221> CDS  
 <222> (1) .. (1374)  
 <223> D6-desaturase

<400> 31		
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Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu		
1 5 10 15		
aat gcc gag gct ctg aat gag ggc aag aag gat gcc gag gca ccc ttc		96
Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe		
20 25 30		
ttg atg atc atc gac aac aag gtg tac gat gtt cgc gag ttc gtc cct		144
Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro		

35	40	45	
gat cat ccc ggt gga agt gtg att ctc acg cac gtt ggc aag gac ggc Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly 50 55 60			192
act gac gtc ttt gac act ttt cac ccc gag gct gct tgg gag act ctt Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu 65 70 75 80			240
gcc aac ttt tac gtt ggt gat att gac gag agc gac cgc gat atc aag Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys 85 90 95			288
aat gat gac ttt gcg gcc gag gtc cgc aag ctg cgt acc ttg ttc cag Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln 100 105 110			336
tct ctt ggt tac tac gat tct tcc aag gca tac tac gcc ttc aag gtc Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val 115 120 125			384
tcg ttc aac ctc tgc atc tgg ggt ttg tcg acg gtc att gtg gcc aag Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys 130 135 140			432
tgg ggc cag acc tcg acc ctc gcc aac gtg ctc tcg gct gcg ctt ttg Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu 145 150 155 160			480
ggt ctg ttc tgg cag cag tgc gga tgg ttg gct cac gac ttt ttg cat Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His 165 170 175			528
cac cag gtc ttc cag gac cgt ttc tgg ggt gat ctt ttc ggc gcc ttc His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe 180 185 190			576
ttg gga ggt gtc tgc cag ggc ttc tcg tcc tcg tgg tgg aag gac aag Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys 195 200 205			624
cac aac act cac cac gcc gcc ccc aac gtc cac ggc gag gat ccc gac His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp 210 215 220			672
att gac acc cac cct ctg ttg acc tgg agt gag cat gcg ttg gag atg Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met 225 230 235 240			720
ttc tcg gat gtc cca gat gag gag ctg acc cgc atg tgg tcg cgt ttc Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe 245 250 255			768
atg gtc ctg aac cag acc tgg ttt tac ttc ccc att ctc tcg ttt gcc Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala 260 265 270			816

cgt ctc tcc tgg tgc ctc cag tcc att ctc ttt gtg ctg cct aac ggt	864
Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly	
275 280 285	
cag gcc cac aag ccc tcg ggc gcg cgt gtg ccc atc tcg ttg gtc gag	912
Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu	
290 295 300	
cag ctg tcg ctt gcg atg cac tgg acc tgg tac ctc gcc acc atg ttc	960
Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe	
305 310 315 320	
ctg ttc atc aag gat ccc gtc aac atg ctg gtg tac ttt ttg gtg tcg	1008
Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser	
325 330 335	
cag gcg gtg tgc gga aac ttg ttg gcg atc gtg ttc tcg ctc aac cac	1056
Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His	
340 345 350	
aac ggt atg cct gtg atc tcg aag gag gag gcg gtc gat atg gat ttc	1104
Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe	
355 360 365	
ttc acg aag cag atc atc acg ggt cgt gat gtc cac ccg ggt cta ttt	1152
Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe	
370 375 380	
gcc aac tgg ttc acg ggt gga ttg aac tat cag atc gag cac cac ttg	1200
Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu	
385 390 395 400	
ttc cct tcg atg cct cgc cac aac ttt tca aag atc cag cct gct gtc	1248
Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val	
405 410 415	
gag acc ctg tgc aaa aag tac aat gtc cga tac cac acc acc ggt atg	1296
Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met	
420 425 430	
atc gag gga act gca gag gtc ttt agc cgt ctg aac gag gtc tcc aag	1344
Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys	
435 440 445	
gct gcc tcc aag atg ggt aag gcg cag taa	1374
Ala Ala Ser Lys Met Gly Lys Ala Gln	
450 455	

&lt;210&gt; 32

&lt;211&gt; 457

&lt;212&gt; PRT

&lt;213&gt; Mortierella alpina

&lt;400&gt; 32

Met Ala Ala Ala Pro Ser Val Arg Thr Phe Thr Arg Ala Glu Val Leu

1	5	10	15
Asn Ala Glu Ala Leu Asn Glu Gly Lys Lys Asp Ala Glu Ala Pro Phe	20	25	30
Leu Met Ile Ile Asp Asn Lys Val Tyr Asp Val Arg Glu Phe Val Pro	35	40	45
Asp His Pro Gly Gly Ser Val Ile Leu Thr His Val Gly Lys Asp Gly	50	55	60
Thr Asp Val Phe Asp Thr Phe His Pro Glu Ala Ala Trp Glu Thr Leu	65	70	75
Ala Asn Phe Tyr Val Gly Asp Ile Asp Glu Ser Asp Arg Asp Ile Lys	85	90	95
Asn Asp Asp Phe Ala Ala Glu Val Arg Lys Leu Arg Thr Leu Phe Gln	100	105	110
Ser Leu Gly Tyr Tyr Asp Ser Ser Lys Ala Tyr Tyr Ala Phe Lys Val	115	120	125
Ser Phe Asn Leu Cys Ile Trp Gly Leu Ser Thr Val Ile Val Ala Lys	130	135	140
Trp Gly Gln Thr Ser Thr Leu Ala Asn Val Leu Ser Ala Ala Leu Leu	145	150	155
Gly Leu Phe Trp Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His	165	170	175
His Gln Val Phe Gln Asp Arg Phe Trp Gly Asp Leu Phe Gly Ala Phe	180	185	190
Leu Gly Gly Val Cys Gln Gly Phe Ser Ser Ser Trp Trp Lys Asp Lys	195	200	205
His Asn Thr His His Ala Ala Pro Asn Val His Gly Glu Asp Pro Asp	210	215	220
Ile Asp Thr His Pro Leu Leu Thr Trp Ser Glu His Ala Leu Glu Met	225	230	235
Phe Ser Asp Val Pro Asp Glu Glu Leu Thr Arg Met Trp Ser Arg Phe	245	250	255
Met Val Leu Asn Gln Thr Trp Phe Tyr Phe Pro Ile Leu Ser Phe Ala	260	265	270
Arg Leu Ser Trp Cys Leu Gln Ser Ile Leu Phe Val Leu Pro Asn Gly	275	280	285
Gln Ala His Lys Pro Ser Gly Ala Arg Val Pro Ile Ser Leu Val Glu	290	295	300
Gln Leu Ser Leu Ala Met His Trp Thr Trp Tyr Leu Ala Thr Met Phe			

305		310		315		320
Leu Phe Ile Lys Asp Pro Val Asn Met Leu Val Tyr Phe Leu Val Ser	325		330		335	
Gln Ala Val Cys Gly Asn Leu Leu Ala Ile Val Phe Ser Leu Asn His	340		345		350	
Asn Gly Met Pro Val Ile Ser Lys Glu Glu Ala Val Asp Met Asp Phe	355		360		365	
Phe Thr Lys Gln Ile Ile Thr Gly Arg Asp Val His Pro Gly Leu Phe	370		375		380	
Ala Asn Trp Phe Thr Gly Gly Leu Asn Tyr Gln Ile Glu His His Leu	385		390		395	400
Phe Pro Ser Met Pro Arg His Asn Phe Ser Lys Ile Gln Pro Ala Val	405		410		415	
Glu Thr Leu Cys Lys Lys Tyr Asn Val Arg Tyr His Thr Thr Gly Met	420		425		430	
Ile Glu Gly Thr Ala Glu Val Phe Ser Arg Leu Asn Glu Val Ser Lys	435		440		445	
Ala Ala Ser Lys Met Gly Lys Ala Gln	450		455			

&lt;210&gt; 33

&lt;211&gt; 3598

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

<223> Sequence constitutes a plant  
promoter-terminator expression cassette in vector  
pUC19

&lt;400&gt; 33

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<210> 34

<211> 3590

<212> DNA

<213> Unknown

<220>

<223> Sequence constitutes a plant  
 promoter-terminator expression cassette in vector  
 pUC19

&lt;400&gt; 34

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<210> 35

<211> 3584

<212> DNA

<213> Unknown

<220>

<223> Sequence constitutes a plant  
 promoter-terminator expression cassette in vector  
 pUC19

<400> 35

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<210> 36

<211> 4507

<212> DNA

<213> Unknown

<220>

<223> Sequence constitutes a plant  
 promoter-terminator expression cassette in vector  
 pUC19

<400> 36

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<210> 37

<211> 5410

<212> DNA

<213> Unknown

<220>

<223> Sequence constitutes a plant  
 promoter-terminator expression cassette in vector  
 pUC19

<400> 37

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<210> 38

<211> 12093

<212> DNA

<213> Unknown

<220>

<223> Plant expression vector with a  
promoter-terminator expression cassette

<400> 38

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Phe Cys Phe Ala Leu Ser Leu Tyr Met Cys Val Gly Ile Ala Tyr Gln	
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His Lys Glu Met Ala Ile Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr	
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Gln Ile Ser Phe Leu His Val Tyr His His Ser Ser Ile Ser Leu Ile	
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Thr	Ile	Ser	Ala	Val	Leu	Ala	Ser	Ala	Cys	Met	Met	Ala	Leu	Cys	Phe		
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Phe	Phe	Met	Gly	Leu	Leu	Phe	Phe	Ala	Arg	Gly	Ser	Trp	Leu	Phe	Trp	
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Phe	Cys	Phe	Ala	Leu	Ser	Leu	Tyr	Met	Cys	Val	Gly	Ile	Ala	Tyr	Gln	
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His Lys Glu Met Ala Ile Leu Val Tyr Leu Phe Tyr Met Ser Lys Tyr	
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Val Glu Phe Met Asp Thr Val Ile Met Ile Leu Lys Arg Ser Thr Arg	
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Gln Ile Ser Phe Leu His Val Tyr His His Ser Ile Ser Leu Ile	
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Trp Trp Ala Ile Ala His His Ala Pro Gly Gly Glu Ala Tyr Trp Ser	
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Ala Ala Leu Asn Ser Gly Val His Val Leu Met Tyr Ala Tyr Tyr Phe	
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Asn Leu Val Gln Ala Tyr Tyr Asp Met Lys Thr Asn Ala Pro Tyr Pro	
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Gln Trp Leu Ile Lys Ile Leu Phe Tyr Tyr Met Ile Ser Leu Leu Phe	
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Ala Ser Met Ser Leu Phe Ser Asp Phe Phe Ser Tyr Val Ser Ser Thr						
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Val Gly Ser Trp Ser Val His Ser Ile Gln Pro Leu Lys Arg Leu Thr						
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agt aag aag cgt gtt tcg gaa agc gct gcc gtg caa tgt ata tca gct						13522
Ser Lys Lys Arg Val Ser Glu Ser Ala Ala Val Gln Cys Ile Ser Ala						
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gaa gtt cag aga aat tcg agt acc cag gga act gcg gag gca ctc gca						13570
Glu Val Gln Arg Asn Ser Ser Thr Gln Gly Thr Ala Glu Ala Leu Ala						
			365		370	375
gaa tca gtc gtg aag ccc acg aga cga agg tca tct cag tgg aag aag						13618
Glu Ser Val Val Lys Pro Thr Arg Arg Arg Ser Ser Gln Trp Lys Lys						
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tcg aca cac ccc cta tca gaa gta gca gta cac aac aag cca agc gat						13666
Ser Thr His Pro Leu Ser Glu Val Ala Val His Asn Lys Pro Ser Asp						
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tcg tgg att gtt gta aaa aac aag gtg tat gat gtt tcc aat ttt gcg						13714
Cys Trp Ile Val Val Lys Asn Lys Val Tyr Asp Val Ser Asn Phe Ala						
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gac gag cat ccc gga gga tca gtt att agt act tat ttt gga cga gac						13762
Asp Glu His Pro Gly Gly Ser Val Ile Ser Thr Tyr Phe Gly Arg Asp						
			430		435	440

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Gly Thr Asp Val Phe Ser Ser Phe His Ala Ala Ser Thr Trp Lys Ile	
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Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu Arg Val Glu Pro Thr Pro	
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Glu Thr Arg Trp Leu Asn Glu Val Val Gly Tyr Val Ile Gly Asn Ala	
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Val Leu Gly Phe Ser Thr Gly Trp Trp Lys Glu Lys His Asn Leu His	
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Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp Ser Lys Asp Ile Leu Ala	
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Thr Val Glu Asn Lys Thr Phe Leu Arg Ile Leu Gln Tyr Gln His Leu	
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Phe Phe Met Gly Leu Leu Phe Phe Ala Arg Gly Ser Trp Leu Phe Trp	
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agc tgg aga tat acc tct aca gca gtg ctc tca cct gtc gac agg ttg	14434
Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu Ser Pro Val Asp Arg Leu	
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Leu Glu Lys Gly Thr Val Leu Phe His Tyr Phe Trp Phe Val Gly Thr	
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Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro Leu Val Trp Met Ala Val	
685 690 695	
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Thr Glu Leu Met Ser Gly Met Leu Leu Gly Phe Val Phe Val Leu Ser	
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His Asn Gly Met Glu Val Tyr Asn Ser Ser Lys Glu Phe Val Ser Ala	
715 720 725	
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Gln Ile Val Ser Thr Arg Asp Ile Lys Gly Asn Ile Phe Asn Asp Trp	
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Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro Thr	
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atg ccc agg cat aat tta aac aaa ata gca cct aga gtg gag gtg ttc	14770
Met Pro Arg His Asn Leu Asn Lys Ile Ala Pro Arg Val Glu Val Phe	
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Cys Lys Lys His Gly Leu Val Tyr Glu Asp Val Ser Ile Ala Thr Gly	
780 785 790	
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Thr Cys Lys Val Leu Lys Ala Leu Lys Glu Val Ala Glu Ala Ala Ala	
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Glu Gln His Ala Thr Thr Ser	
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Ser Thr Gln Glu Arg Leu Cys Ser Leu Ser Ser Leu Lys Gly Glu Glu						
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Val Cys Ile Asp Gly Ile Ile Tyr Asp Leu Gln Ser Phe Asp His Pro						
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Gly Gly Glu Thr Ile Lys Met Phe Gly Gly Asn Asp Val Thr Val Gln						
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tac aag atg att cac ccg tac cat acc gag aag cat ttg gaa aag atg						16054
Tyr Lys Met Ile His Pro Tyr His Thr Glu Lys His Leu Glu Lys Met						
		890		895	900	905
aag cgt gtc ggc aag gtg acg gat ttc gtc tgc gag tac aag ttc gat						16102
Lys Arg Val Gly Lys Val Thr Asp Phe Val Cys Glu Tyr Lys Phe Asp						
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Thr Glu Phe Glu Arg Glu Ile Lys Arg Glu Val Phe Lys Ile Val Arg						
		925		930	935	
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Arg Gly Lys Asp Phe Gly Thr Leu Gly Trp Phe Phe Arg Ala Phe Cys						
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Tyr Ile Ala Ile Phe Phe Tyr Leu Gln Tyr His Trp Val Thr Thr Gly						
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Thr Ser Trp Leu Leu Ala Val Ala Tyr Gly Ile Ser Gln Ala Met Ile						
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Gly Met Asn Val Gln His Asp Ala Asn His Gly Ala Thr Ser Lys Arg						

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tcc aag tgg ctc tgg cag gaa caa cac tgg acc cac cac gct tac acc Ser Lys Trp Leu Trp Gln Glu Gln His Trp Thr His His Ala Tyr Thr 1020 1025 1030			16438
aat cac gcc gag atg gat ccc gat agc ttt ggt gcc gaa cca atg ctc Asn His Ala Glu Met Asp Pro Asp Ser Phe Gly Ala Glu Pro Met Leu 1035 1040 1045			16486
cta ttc aac gac tat ccc ttg gat cat ccc gct cgt acc tgg cta cat Leu Phe Asn Asp Tyr Pro Leu Asp His Pro Ala Arg Thr Trp Leu His 1050 1055 1060 1065			16534
cgc ttt caa gca ttc ttt tac atg ccc gtc ttg gct gga tac tgg ttg Arg Phe Gln Ala Phe Phe Tyr Met Pro Val Leu Ala Gly Tyr Trp Leu 1070 1075 1080			16582
tcc gct gtc ttc aat cca caa att ctt gac ctc cag caa cgc ggc gca Ser Ala Val Phe Asn Pro Gln Ile Leu Asp Leu Gln Gln Arg Gly Ala 1085 1090 1095			16630
ctt tcc gtc ggt atc cgt ctc gac aac gct ttc att cac tcg cga cgc Leu Ser Val Gly Ile Arg Leu Asp Asn Ala Phe Ile His Ser Arg Arg 1100 1105 1110			16678
aag tat gcg gtt ttc tgg cgg gct gtg tac att gcg gtg aac gtg att Lys Tyr Ala Val Phe Trp Arg Ala Val Tyr Ile Ala Val Asn Val Ile 1115 1120 1125			16726
gct ccg ttt tac aca aac tcc ggc ctc gaa tgg tcc tgg cgt gtc ttt Ala Pro Phe Tyr Thr Asn Ser Gly Leu Glu Trp Ser Trp Arg Val Phe 1130 1135 1140 1145			16774
gga aac atc atg ctc atg ggt gtg gcg gaa tcg ctc gcg ctg gcg gtc Gly Asn Ile Met Leu Met Gly Val Ala Glu Ser Leu Ala Leu Ala Val 1150 1155 1160			16822
ctg ttt tcg ttg tcg cac aat ttc gaa tcc gcg gat cgc gat ccg acc Leu Phe Ser Leu Ser His Asn Phe Glu Ser Ala Asp Arg Asp Pro Thr 1165 1170 1175			16870
gcc cca ctg aaa aag acg gga gaa cca gtc gac tgg ttc aag aca cag Ala Pro Leu Lys Lys Thr Gly Glu Pro Val Asp Trp Phe Lys Thr Gln 1180 1185 1190			16918
gtc gaa act tcc tgc act tac ggt gga ttc ctt tcc ggt tgc ttc acg Val Glu Thr Ser Cys Thr Tyr Gly Gly Phe Leu Ser Gly Cys Phe Thr 1195 1200 1205			16966
gga ggt ctc aac ttt cag gtt gaa cac cac ttg ttc cca cgc atg agc Gly Gly Leu Asn Phe Gln Val Glu His His Leu Phe Pro Arg Met Ser 1210 1215 1220 1225			17014

agc gct tgg tat ccc tac att gcc ccc aag gtc cgc gaa att tgc gcc 17062  
 Ser Ala Trp Tyr Pro Tyr Ile Ala Pro Lys Val Arg Glu Ile Cys Ala  
                   1230                  1235                  1240

aaa cac ggc gtc cac tac gcc tac tac ccg tgg atc cac caa aac ttt 17110  
 Lys His Gly Val His Tyr Ala Tyr Tyr Pro Trp Ile His Gln Asn Phe  
                   1245                  1250                  1255

ctc tcc acc gtc cgc tac atg cac gcg gcc ggg acc ggt gcc aac tgg 17158  
 Leu Ser Thr Val Arg Tyr Met His Ala Ala Gly Thr Gly Ala Asn Trp  
                   1260                  1265                  1270

cgc cag atg gcc aga gaa aat ccc ttg acc gga cgg gcg taa 17200  
 Arg Gln Met Ala Arg Glu Asn Pro Leu Thr Gly Arg Ala  
                   1275                  1280                  1285

agatctgccg gcatcgatcc cgggccatgg cctgctttaa tgagatatgc gagacgccta 17260

tgatcgcatg atatttgctt tcaattctgt tgtgcacggt gtaaaaaacc tgagcatgtg 17320

tagctcagat ccttaccgcc ggtttcgggt cattctaata aatatatcac ccgttactat 17380

cgtattttta tgaataatat tctccgttca atttactgat tgtccgtcga cgagctcggc 17440

gcgcctctag aggatcgatg aattcagatc ggctgagtgg ctccttcaac gttgcgggtc 17500

tgtcagttcc aaacgtaaaa cggcttgctc cgcgtcatcg gcgggggtca taacgtgact 17560

cccttaattc tccgctcatg atcagattgt cgtttccgc cttcagttta aactatcagt 17620

gtttgacagg atatattggc gggtaaacct aagagaaaag agcgtttatt agaataatcg 17680

gatatttaaa agggcgtgaa aaggtttatc cttcgtccat ttgtatgtgc atgccaacca 17740

cagggttccc ca 17752

<210> 47

<211> 290

<212> PRT

<213> Unknown

<400> 47

Met Glu Val Val Glu Arg Phe Tyr Gly Glu Leu Asp Gly Lys Val Ser  
           1                  5                  10                  15

Gln Gly Val Asn Ala Leu Leu Gly Ser Phe Gly Val Glu Leu Thr Asp  
                   20                  25                  30

Thr Pro Thr Thr Lys Gly Leu Pro Leu Val Asp Ser Pro Thr Pro Ile  
           35                  40                  45

Val Leu Gly Val Ser Val Tyr Leu Thr Ile Val Ile Gly Gly Leu Leu  
           50                  55                  60

Trp Ile Lys Ala Arg Asp Leu Lys Pro Arg Ala Ser Glu Pro Phe Leu



65	70	75	80
Leu Gln Ala	Leu Val	Leu Val His Asn	Leu Phe Cys Phe Ala Leu Ser
	85	90	95
Leu Tyr Met	Cys Val Gly Ile	Ala Tyr Gln Ala Ile Thr	Trp Arg Tyr
	100	105	110
Ser Leu Trp	Gly Asn Ala Tyr	Asn Pro Lys His Lys	Glu Met Ala Ile
	115	120	125
Leu Val Tyr	Leu Phe Tyr	Met Ser Lys Tyr	Val Glu Phe Met Asp Thr
	130	135	140
Val Ile Met	Ile Leu Lys Arg	Ser Thr Arg	Gln Ile Ser Phe Leu His
	145	150	155
Val Tyr His	His Ser Ser Ile	Ser Leu Ile Trp	Trp Ala Ile Ala His
	165	170	175
His Ala Pro	Gly Gly Glu Ala Tyr	Trp Ser Ala Ala	Leu Asn Ser Gly
	180	185	190
Val His Val	Leu Met Tyr Ala Tyr	Tyr Phe Leu Ala	Ala Cys Leu Arg
	195	200	205
Ser Ser Pro	Lys Leu Lys Asn Lys Tyr	Leu Phe Trp Gly	Arg Tyr Leu
	210	215	220
Thr Gln Phe	Gln Met Phe Gln Phe Met	Leu Asn Leu Val	Gln Ala Tyr
	225	230	235
Tyr Asp Met	Lys Thr Asn Ala Pro Tyr	Pro Gln Trp Leu Ile	Lys Ile
	245	250	255
Leu Phe Tyr	Tyr Met Ile Ser Leu	Leu Phe Leu Phe Gly	Asn Phe Tyr
	260	265	270
Val Gln Lys	Tyr Ile Lys Pro Ser Asp	Gly Lys Gln Lys Gly	Ala Lys
	275	280	285
Thr Glu			
	290		
<210> 48			
<211> 525			
<212> PRT			
<213> Unknown			
<400> 48			
Met Val Phe	Ala Gly Gly Gly	Leu Gln Gln Gly	Ser Leu Glu Glu Asn
1	5	10	15
Ile Asp Val	Glu His Ile Ala Ser	Met Ser Leu Phe Ser	Asp Phe Phe
	20	25	30

Ser Tyr Val Ser Ser Thr Val Gly Ser Trp Ser Val His Ser Ile Gln  
 35 40 45  
 Pro Leu Lys Arg Leu Thr Ser Lys Lys Arg Val Ser Glu Ser Ala Ala  
 50 55 60  
 Val Gln Cys Ile Ser Ala Glu Val Gln Arg Asn Ser Ser Thr Gln Gly  
 65 70 75 80  
 Thr Ala Glu Ala Leu Ala Glu Ser Val Val Lys Pro Thr Arg Arg Arg  
 85 90 95  
 Ser Ser Gln Trp Lys Lys Ser Thr His Pro Leu Ser Glu Val Ala Val  
 100 105 110  
 His Asn Lys Pro Ser Asp Cys Trp Ile Val Val Lys Asn Lys Val Tyr  
 115 120 125  
 Asp Val Ser Asn Phe Ala Asp Glu His Pro Gly Gly Ser Val Ile Ser  
 130 135 140  
 Thr Tyr Phe Gly Arg Asp Gly Thr Asp Val Phe Ser Ser Phe His Ala  
 145 150 155 160  
 Ala Ser Thr Trp Lys Ile Leu Gln Asp Phe Tyr Ile Gly Asp Val Glu  
 165 170 175  
 Arg Val Glu Pro Thr Pro Glu Leu Leu Lys Asp Phe Arg Glu Met Arg  
 180 185 190  
 Ala Leu Phe Leu Arg Glu Gln Leu Phe Lys Ser Ser Lys Leu Tyr Tyr  
 195 200 205  
 Val Met Lys Leu Leu Thr Asn Val Ala Ile Phe Ala Ala Ser Ile Ala  
 210 215 220  
 Ile Ile Cys Trp Ser Lys Thr Ile Ser Ala Val Leu Ala Ser Ala Cys  
 225 230 235 240  
 Met Met Ala Leu Cys Phe Gln Gln Cys Gly Trp Leu Ser His Asp Phe  
 245 250 255  
 Leu His Asn Gln Val Phe Glu Thr Arg Trp Leu Asn Glu Val Val Gly  
 260 265 270  
 Tyr Val Ile Gly Asn Ala Val Leu Gly Phe Ser Thr Gly Trp Trp Lys  
 275 280 285  
 Glu Lys His Asn Leu His His Ala Ala Pro Asn Glu Cys Asp Gln Thr  
 290 295 300  
 Tyr Gln Pro Ile Asp Glu Asp Ile Asp Thr Leu Pro Leu Ile Ala Trp  
 305 310 315 320  
 Ser Lys Asp Ile Leu Ala Thr Val Glu Asn Lys Thr Phe Leu Arg Ile  
 325 330 335

Leu Gln Tyr Gln His Leu Phe Phe Met Gly Leu Leu Phe Phe Ala Arg  
                   340                                  345                                  350  
 Gly Ser Trp Leu Phe Trp Ser Trp Arg Tyr Thr Ser Thr Ala Val Leu  
                   355                                  360                                  365  
 Ser Pro Val Asp Arg Leu Leu Glu Lys Gly Thr Val Leu Phe His Tyr  
                   370                                  375                                  380  
 Phe Trp Phe Val Gly Thr Ala Cys Tyr Leu Leu Pro Gly Trp Lys Pro  
                   385                                  390                                  395                                  400  
 Leu Val Trp Met Ala Val Thr Glu Leu Met Ser Gly Met Leu Leu Gly  
                                   405                                  410                                  415  
 Phe Val Phe Val Leu Ser His Asn Gly Met Glu Val Tyr Asn Ser Ser  
                   420                                  425                                  430  
 Lys Glu Phe Val Ser Ala Gln Ile Val Ser Thr Arg Asp Ile Lys Gly  
                   435                                  440                                  445  
 Asn Ile Phe Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu  
                   450                                  455                                  460  
 His His Leu Phe Pro Thr Met Pro Arg His Asn Leu Asn Lys Ile Ala  
                   465                                  470                                  475                                  480  
 Pro Arg Val Glu Val Phe Cys Lys Lys His Gly Leu Val Tyr Glu Asp  
                                   485                                  490                                  495  
 Val Ser Ile Ala Thr Gly Thr Cys Lys Val Leu Lys Ala Leu Lys Glu  
                   500                                  505                                  510  
 Val Ala Glu Ala Ala Ala Glu Gln His Ala Thr Thr Ser  
                   515                                  520                                  525

<210> 49  
 <211> 469  
 <212> PRT  
 <213> Unknown

<400> 49  
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 Ala Lys His Asn Ala Ala Thr Ile Ser Thr Gln Glu Arg Leu Cys Ser  
                   20                                  25                                  30  
 Leu Ser Ser Leu Lys Gly Glu Glu Val Cys Ile Asp Gly Ile Ile Tyr  
                   35                                  40                                  45  
 Asp Leu Gln Ser Phe Asp His Pro Gly Gly Glu Thr Ile Lys Met Phe  
                   50                                  55                                  60  
 Gly Gly Asn Asp Val Thr Val Gln Tyr Lys Met Ile His Pro Tyr His  
                   65                                  70                                  75                                  80

Thr	Glu	Lys	His	Leu	Glu	Lys	Met	Lys	Arg	Val	Gly	Lys	Val	Thr	Asp	85	90	95	
Phe	Val	Cys	Glu	Tyr	Lys	Phe	Asp	Thr	Glu	Phe	Glu	Arg	Glu	Ile	Lys	100	105	110	
Arg	Glu	Val	Phe	Lys	Ile	Val	Arg	Arg	Gly	Lys	Asp	Phe	Gly	Thr	Leu	115	120	125	
Gly	Trp	Phe	Phe	Arg	Ala	Phe	Cys	Tyr	Ile	Ala	Ile	Phe	Phe	Tyr	Leu	130	135	140	
Gln	Tyr	His	Trp	Val	Thr	Thr	Gly	Thr	Ser	Trp	Leu	Leu	Ala	Val	Ala	145	150	155	160
Tyr	Gly	Ile	Ser	Gln	Ala	Met	Ile	Gly	Met	Asn	Val	Gln	His	Asp	Ala	165	170	175	
Asn	His	Gly	Ala	Thr	Ser	Lys	Arg	Pro	Trp	Val	Asn	Asp	Met	Leu	Gly	180	185	190	
Leu	Gly	Ala	Asp	Phe	Ile	Gly	Gly	Ser	Lys	Trp	Leu	Trp	Gln	Glu	Gln	195	200	205	
His	Trp	Thr	His	His	Ala	Tyr	Thr	Asn	His	Ala	Glu	Met	Asp	Pro	Asp	210	215	220	
Ser	Phe	Gly	Ala	Glu	Pro	Met	Leu	Leu	Phe	Asn	Asp	Tyr	Pro	Leu	Asp	225	230	235	240
His	Pro	Ala	Arg	Thr	Trp	Leu	His	Arg	Phe	Gln	Ala	Phe	Phe	Tyr	Met	245	250	255	
Pro	Val	Leu	Ala	Gly	Tyr	Trp	Leu	Ser	Ala	Val	Phe	Asn	Pro	Gln	Ile	260	265	270	
Leu	Asp	Leu	Gln	Gln	Arg	Gly	Ala	Leu	Ser	Val	Gly	Ile	Arg	Leu	Asp	275	280	285	
Asn	Ala	Phe	Ile	His	Ser	Arg	Arg	Lys	Tyr	Ala	Val	Phe	Trp	Arg	Ala	290	295	300	
Val	Tyr	Ile	Ala	Val	Asn	Val	Ile	Ala	Pro	Phe	Tyr	Thr	Asn	Ser	Gly	305	310	315	320
Leu	Glu	Trp	Ser	Trp	Arg	Val	Phe	Gly	Asn	Ile	Met	Leu	Met	Gly	Val	325	330	335	
Ala	Glu	Ser	Leu	Ala	Leu	Ala	Val	Leu	Phe	Ser	Leu	Ser	His	Asn	Phe	340	345	350	
Glu	Ser	Ala	Asp	Arg	Asp	Pro	Thr	Ala	Pro	Leu	Lys	Lys	Thr	Gly	Glu	355	360	365	
Pro	Val	Asp	Trp	Phe	Lys	Thr	Gln	Val	Glu	Thr	Ser	Cys	Thr	Tyr	Gly	370	375	380	

Gly Phe Leu Ser Gly Cys Phe Thr Gly Gly Leu Asn Phe Gln Val Glu  
385 390 395 400

His His Leu Phe Pro Arg Met Ser Ser Ala Trp Tyr Pro Tyr Ile Ala  
405 410 415

Pro Lys Val Arg Glu Ile Cys Ala Lys His Gly Val His Tyr Ala Tyr  
420 425 430

Tyr Pro Trp Ile His Gln Asn Phe Leu Ser Thr Val Arg Tyr Met His  
435 440 445

Ala Ala Gly Thr Gly Ala Asn Trp Arg Gln Met Ala Arg Glu Asn Pro  
450 455 460

Leu Thr Gly Arg Ala  
465

<210> 50

<211> 26

<212> DNA

<213> Artificial sequence

<220>

<223> Polylinker

<400> 50

gaattcggcg cgccgagctc ctcgag

26

<210> 51

<211> 265

<212> DNA

<213> Artificial sequence

<220>

<223> Polylinker-terminator-polylinker

<400> 51

ccaccgcggt gggcggccgc ctgcagtcta gaaggcctcc tgctttaatg agatatgcga 60

gacgcctatg atcgcatgat atttgctttc aattctgttg tgcacgttgt aaaaaacctg 120

agcatgtgta gctcagatcc ttaccgccgg ttccggttca ttctaataa tatatcaccc 180

gttactatcg tatttttatg aataatattc tccgttcaat ttactgattg tccgtcgacg 240

aattcgagct cggcgcgcca agctt

265

<210> 52

<211> 257

<212> DNA

<213> Artificial sequence

&lt;220&gt;

&lt;223&gt; Polylinker-terminator-polylinker

&lt;400&gt; 52

ggatccgata tcgggccgcg tagcggttaac cctgctttaa tgagatatgc gagacgccta 60  
tgatcgcgatg atatttgctt tcaattctgt tgtgcacggt gtaaaaaacc tgagcatgtg 120  
tagctcagat ccttaccgcc ggtttcgggt cattctaata aatatatcac ccgttactat 180  
cgtattttta tgaataatat tctccgttca atttactgat tgtccgtcga cgaattcgag 240  
ctcggcgcgc caagctt 257

&lt;210&gt; 53

&lt;211&gt; 257

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Polylinker-terminator-polylinker

&lt;400&gt; 53

agatctgccg gcatcgatcc cgggccatgg cctgctttaa tgagatatgc gagacgccta 60  
tgatcgcgatg atatttgctt tcaattctgt tgtgcacggt gtaaaaaacc tgagcatgtg 120  
tagctcagat ccttaccgcc ggtttcgggt cattctaata aatatatcac ccgttactat 180  
cgtattttta tgaataatat tctccgttca atttactgat tgtccgtcga cgaattcgag 240  
ctcggcgcgc caagctt 257

□